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FIME HEAPLUS, MEDLINE, BIOSIS, EMBASE, WPIDS, CONFSCI, SCISEARCH,
     JICST-EPLUS, JAPIO' ENTERED AT 10:37:11 ON 28 JAN 2003
                                                                       Duther (5)
             584 S "BURNIE J"?/AU
 L1
            5349 S "MATTHEWS R"?/AU
 L2
             326 S L1 AND L2
 L3
              45 S (L3 OR L1 OR L2) AND PNEUMON?
Ji4
            21 DUP REM L4 (24 DUPLICATES REMOVED) >
                      HCAPLUS COPYRIGHT 2003 ACS
                                                         DUPLICATE 1
 L5
      ANSWER 1 OF 21
                          2000:553692 HCAPLUS
 ACCESSION NUMBER:
 DOCUMENT NUMBER:
                          133:145931
                          Protein and DNA sequences of a novel Chlamydia
 TITLE:
                          pneumoniae antigen and the uses in
                          diagnosis and treatment of deseases associated
                          with Chlamydia infection
                          Burnie, James Peter; Matthews,
 INVENTOR(S):
                          Ruth Christine
                          Neutec Pharma Plc, UK
 PATENT ASSIGNEE(S):
                          PCT Int. Appl., 35 pp.
 SOURCE:
                          CODEN: PIXXD2
 DOCUMENT TYPE:
                          Patent
                          English
 LANGUAGE:
 FAMILY ACC. NUM. COUNT:
                          1
 PATENT INFORMATION:
                                            APPLICATION NO.
                                                              DATE
                             DATE
      PATENT NO.
                       KIND
                                            _____
                             _____
                       ____
                             20000810
                                            WO 2000-GB237
                                                              20000128
                        A2
      WO 2000046359
                             20001207
                        A3
      WO 2000046359
              AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR,
              CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU,
              ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT,
              LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU,
              SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ,
              VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
          RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY,
              DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF,
              BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
                        A2
                             20011031
                                            EP 2000-901235
                                                              20000128
      EP 1149162
              AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC,
              PT, IE, FI
                                          GB 1999-2555
                                                           A 19990205
 PRIORITY APPLN. INFO .:
                                          WO 2000-GB237
                                                          W 20000128
      The invention provides protein and DNA sequences of a novel
 AΒ
      Chlamydia pneumoniae antigen. The present invention
      further relates to the uses of the antigens of this invention in
      treatment, prevention and diagnosis of infection due to Chlamydia
      pneumoniae and in particular to the prevention and treatment
      of atherosclerosis, including coronary atherosclerosis, caused by
      same.
      ANSWER 2 OF 21 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
 L5
                     1999:126671 BIOSIS
 ACCESSION NUMBER:
                     PREV199900126671
 DOCUMENT NUMBER:
                     Is infection control an academic study.
 TITLE:
                     Burnie, J. P. (1)
 AUTHOR(S):
                     (1) Dep. Med. Microbiol., 2nd Floor, Clin. Sci.
 CORPORATE SOURCE:
                     Build., Manchester Royal Infirmary, Oxford Road,
```

Manchester M13 9WL UK

Journal of Hospital Infection, (Jan., 1999) Vol. 41, SOURCE:

No. 1, pp. 7-10. ISSN: 0195-6701.

DOCUMENT TYPE: Editorial

LANGUAGE: English AΒ

This editorial aims to answer the question of whether infection control is an academic specialty. By considering the consequences of a lack of infection control in terms of patient morbidity and mortality and hence cost, it is easy to establish the importance of the area. Infection control embraces not only developing policies for preventing the physical spread of a microorganism but also prophylactic therapy such as vaccination and therapeutic measures such as antibiotics. Infection control not only applies to localized infection in hospital due to antibiotic resistant microbes but also to the community. Bacteria such as Helicobacter pylori and Chlamydia pneumoniae and the viruses Hepatitis B, Hepatitis C, human lymphotropic virus type 1, Epstein-Barr viruses and human papilloma virus have been implicated in diseases not previously thought to have an infectious origin. Coping with these problems is clearly an academic area.

DUPLICATE 2 ANSWER 3 OF 21 MEDLINE

ACCESSION NUMBER: 2000028548 MEDLINE

DOCUMENT NUMBER: 20028548 PubMed ID: 10562808

A polymerase chain reaction enzyme immunoassay for TITLE:

diagnosing infection caused by Aspergillus fumigatus.

Golbang N; Burnie J P; Matthews R C AUTHOR:

Department of Medical Microbiology, Manchester CORPORATE SOURCE:

University, Manchester Royal Infirmary, UK.

SOURCE: JOURNAL OF CLINICAL PATHOLOGY, (1999 Jun) 52 (6)

419-23.

Journal code: 0376601. ISSN: 0021-9746.

ENGLAND: United Kingdom PUB. COUNTRY:

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

Abridged Index Medicus Journals; Priority Journals FILE SEGMENT:

ENTRY MONTH: 199911

Entered STN: 20000111 ENTRY DATE:

Last Updated on STN: 20000111 Entered Medline: 19991116

AIM: To develop a polymerase chain reaction enzyme immunoassay AB (PCR-EIA) to measure levels of circulating aspergillus DNA in invasive aspergillosis caused by Aspergillus fumigatus. METHODS: The PCR reaction was based on primers from the 18s rRNA gene. Binding of the product to a streptavidin coated microtitration plate was mediated by a biotinylated capture probe. The product was digoxigenylated during PCR and this was the tag to which antibody was bound in the subsequent EIA. RESULTS: The optical density (OD) endpoint was < 0.1 in 10 sera from neutropenic patients with no evidence of invasive aspergillosis, and in 10 sera from nonneutropenic patients with bacterial pneumonia (group 1). The OD from five of 12 patients with allergic bronchopulmonary aspergillosis (ABPA) (group 2), three with an aspergilloma (group 3), and five with possible invasive aspergillosis (group 4) was > or = 0.1. In 63 sera from 33 cases of proven invasive aspergillosis (group 5) an OD > or = 0.1 was achieved in 48 sera from 30 patients. The maximum OD was 0.510. The level fell in survivors and gradually

> 308-4994 Searcher : Shears

rose in fatal cases. CONCLUSIONS: This assay validated the concept of diagnosing invasive aspergillosis by measuring levels of circulating fungal DNA in serum.

DUPLICATE 3 ANSWER 4 OF 21 MEDLINE **I**:5

1999135117 MEDLINE ACCESSION NUMBER:

DOCUMENT NUMBER: 99135117 PubMed ID: 9949958

Is infection control an academic study?. TITLE:

Burnie J P AUTHOR:

CORPORATE SOURCE: Department of Medical Microbiology, Manchester Royal

Infirmary.

JOURNAL OF HOSPITAL INFECTION, (1999 Jan) 41 (1) SOURCE:

7-10. Ref: 30

Journal code: 8007166. ISSN: 0195-6701.

ENGLAND: United Kingdom

PUB. COUNTRY:

Journal; Article; (JOURNAL ARTICLE) DOCUMENT TYPE:

General Review; (REVIEW)

(REVIEW, TUTORIAL)

LANGUAGE: English

Priority Journals FILE SEGMENT:

ENTRY MONTH: 199904

Entered STN: 19990426 ENTRY DATE:

Last Updated on STN: 19990426 Entered Medline: 19990413

This editorial aims to answer the question of whether infection AB control is an academic specialty. By considering the consequences of a lack of infection control in terms of patient morbidity and mortality and hence cost, it is easy to establish the importance of the area. Infection control embraces not only developing policies for preventing the physical spread of a micro-organism but also prophylactic therapy such as vaccination and therapeutic measures such as antibiotics. Infection control not only applies to localized infection in hospital due to antibiotic resistant microbes but also to the community. Bacteria such as Helicobacter pylori and Chlamydia pneumoniae and the viruses hepatitis B, hepatitis C, human lymphotropic virus type 1, Epstein-Barr viruses and human papilloma virus have been implicated in diseases not previously thought to have an infectious origin. Coping with these problems is clearly an academic area.

ANSWER 5 OF 21 EMBASE COPYRIGHT 2003 ELSEVIER SCI. B.V.

97018133 EMBASE ACCESSION NUMBER:

1997018133 DOCUMENT NUMBER:

Cervical cancer as an AIDS-defining illness. TITLE:

Maiman M.; Fruchter R.G.; Clark M.; Arrastia C.D.; AUTHOR:

Matthews R.; Gates E.J.

Dr. M. Maiman, Division of Gynecologic Oncology, CORPORATE SOURCE:

Department of Obstetrics/Gynecology, SUNY-Health Science Center, 450 Clarkson Avenue, Brooklyn, NY

11203, United States

Obstetrics and Gynecology, (1997) 89/1 (76-80). SOURCE:

Refs: 19

ISSN: 0029-7844 CODEN: OBGNAS

S 0029-7844(96)00378-X PUBLISHER IDENT .:

United States COUNTRY:

DOCUMENT TYPE: Journal; Article Microbiology FILE SEGMENT: 004

010 Obstetrics and Gynecology

016 Cancer

017 Public Health, Social Medicine and

Epidemiology

LANGUAGE: English SUMMARY LANGUAGE: English

Objective: To evaluate the importance of cervical cancer in the spectrum of human immunodeficiency virus (HIV) related diseases at a single high-risk institution and to compare disease characteristics in HIV-infected women with cervical cancer and those with other AIDS-related malignancies. Methods: We retrospectively reviewed data on cervical cancer and AIDS in women registered through the New York City Department of Health and institutional tumor registries from 1987 through 1995. Results: During the study period, cervical cancer was diagnosed in 28 HIV-positive women. In 26, cervical cancer was the initial AIDS-defining illness, representing 4% (26 of 725) of the subjects, and it was the sixth most common initial AIDS-defining illness in women. Cervical cancer was the most common AIDS-related malignancy among women, representing 55% of the cases, followed by lymphoma (29%) and Kaposi sarcoma (16%). In 71% of the women with cervical cancer, HIV infection was diagnosed at the time of cancer presentation by routine testing, whereas in women with other malignancies, HIV diagnosis preceded cancer diagnosis (70%) by a mean of 2.7 years. Patients with other malignancies had greater immunosuppression (mean CD4 count 153/.mu.L) than those with cervical cancer (mean CD4 count 312/.mu.L). The recurrence rate for women with cervical cancer was 88%. Although the interval from cancer diagnosis to death was similar in all three groups (9.1-12.4 months), cancer was the cause of death in 95% of HIV- infected women with cervical cancer, compared with 60% of those with other AIDS-related malignancies. Conclusion: In urban populations at increased risk for both diseases, cervical cancer is an important AIDS-defining illness and may be the most common AIDS-related malignancy in women.

L5 ANSWER 6 OF 21 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 1996:109315 BIOSIS DOCUMENT NUMBER: PREV199698681450

TITLE: Immunoblotting in the diagnosis of culture negative

endocarditis caused by streptococci and enterococci.

AUTHOR(S): Burnie, J. P. (1); Clark, I.

CORPORATE SOURCE: (1) Dep. Medical Microbiol., 2nd Floor, Clinical Sci.

Build., Manchester Royal Infirmary, Oxford Road,

Manchester M13 9WL UK

SOURCE: Journal of Clinical Pathology (London), (1995) Vol.

48, No. 12, pp. 1130-1136.

ISSN: 0021-9746.

DOCUMENT TYPE: Article LANGUAGE: English

AB Aim: To improve the diagnosis of culture negative endocarditis by diagnosing cases due to streptococci and enterococci. Method: Serum samples were immunoblotted against extracts of the commonest streptococci and enterococci. They were selected from patients with a cardiac murmur, persistent pyrexia and at least three negative blood cultures. The presence of patterns of endocarditis species specific antigenic bands was measured and correlated with clinical outcome. Results: Negative serology was found in 28 patients where the diagnosis of endocarditis was rejected or, if proved, staphylococcal, yeast, Gram negative, systemic lupus erythematosus,

due to Q fever or Chlamydia psittaci or nonbacterial thrombotic. Positive serology was found in 27 of the 34 patients where the response to antibiotics suggested streptococcal or enterococcal infection. In 22 of these there was objective evidence of endocarditis. Positive serology was also found in three of four further patients with vegetations at necropsy. Conclusion: The identification of patterns of antibody response on immunoblotting can be used to make a specific diagnosis of streptococcal or enterococcal endocarditis in the absence of positive blood cultures.

5 ANSWER 7 OF 21 SCISEARCH COPYRIGHT 2003 ISI (R)

ACCESSION NUMBER: 94:539953 SCISEARCH

THE GENUINE ARTICLE: PE730

TITLE: THE LEUCINE-RESPONSIVE REGULATORY PROTEIN, A GLOBAL

REGULATOR OF METABOLISM IN ESCHERICHIA-COLI

AUTHOR: CALVO J M (Reprint); MATTHEWS R G

CORPORATE SOURCE: CORNELL UNIV, BIOCHEM MOLEC & CELL BIOL SECT,

ITHACA, NY, 14853 (Reprint); UNIV MICHIGAN, DIV BIOPHYS RES, ANN ARBOR, MI, 48109; UNIV MICHIGAN,

DEPT BIOL CHEM, ANN ARBOR, MI, 48109

COUNTRY OF AUTHOR: USA

SOURCE: MICROBIOLOGICAL REVIEWS, (SEP 1994) Vol. 58, No. 3,

pp. 466-490. ISSN: 0146-0749.

DOCUMENT TYPE: General Review; Journal

FILE SEGMENT: LIFE
LANGUAGE: ENGLISH
REFERENCE COUNT: 187

\*ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS\* Natural genetic transformation is the active uptake of free DNA AΒ by bacterial cells and the heritable incorporation of its genetic information. Since the famous discovery of transformation in Streptococcus pneumoniae by Griffith in 1928 and the demonstration of DNA as the transforming principle by Avery and coworkers in 1944, cellular processes involved in transformation have been studied extensively by in vitro experimentation with a few transformable species. Only more recently has it been considered that transformation may be a powerful mechanism of horizontal gene transfer in natural bacterial populations. In this review the current understanding of the biology of transformation is summarized to provide the platform on which aspects of bacterial transformation in water soil, and sediments and the habitat of pathogens are discussed. Direct and indirect evidence for gene transfer routes by transformation within species and between different species will be presented, along with data suggesting that plasmids as well as chromosomal DNA are subject to genetic exchange via transformation. Experiments exploring the prerequisites for transformation in the environment, including the production and persistence of free DNA and factors important for the uptake of DNA by cells, will be compiled, as well as possible natural barriers to transformation. The efficiency of gene transfer by transformation in bacterial habitats is possibly genetically adjusted to submaximal levels. The fact that natural transformation has been detected among bacteria from all trophic and taxonomic groups including archaebacteria suggests that transformability evolved early in phylogeny. Probable functions of DNA uptake other than gene acquisition will be discussed. The body of information presently available suggests that

Searcher: Shears 308-4994

transformation has a great impact on bacterial population dynamics

as well as on bacterial evolution and speciation.

L5 ANSWER 8 OF 21 SCISEARCH COPYRIGHT 2003 ISI (R)

ACCESSION NUMBER: 92:717086 SCISEARCH

THE GENUINE ARTICLE: KA952

TITLE: PROGRESSIVE CHRONIC PULMONARY ASPERGILLOSIS - A

DIAGNOSTIC AND THERAPEUTIC CHALLENGE

AUTHOR: ELLIS M E (Reprint); DOSSING M; ALHOKAIL A; QADRI S

H; HAINAU B; BURNIE J

CORPORATE SOURCE: KING FAISAL SPECIALIST HOSP & RES CTR, DEPT MED, MBC

46, POB 3354, RIYADH 11211, SAUDI ARABIA (Reprint); KING FAISAL SPECIALIST HOSP & RES CTR, DEPT PATHOL &

LAB MED, RIYADH 11211, SAUDI ARABIA; UNIV

MANCHESTER, SCH MED, DEPT MICROBIOL, MANCHESTER M13

9PL, LANCS, ENGLAND

COUNTRY OF AUTHOR: SAUDI ARABIA; ENGLAND

COUNTRY OF AUTHOR: SAUDI ARABIA; ENGLAND

SOURCE: JOURNAL OF THE ROYAL SOCIETY OF MEDICINE, (DEC 1992)

Vol. 85, No. 12, pp. 763-764.

ISSN: 0141-0768.

DOCUMENT TYPE: Article; Journal

FILE SEGMENT: LIFE; CLIN LANGUAGE: ENGLISH

REFERENCE COUNT: 13

L5 ANSWER 9 OF 21 HCAPLUS COPYRIGHT 2003 ACS DUPLICATE 4

ACCESSION NUMBER: 1992:507995 HCAPLUS

DOCUMENT NUMBER: 117:107995

TITLE: The in vitro activity of two new quinolones:

rufloxacin and MF 961

AUTHOR(S): Wise, R.; Andrews, J. M.; Matthews, R.

; Wolstenholme, M.

CORPORATE SOURCE: Dep. Med. Microbiol., Dudley Road Hosp.,

Birmingham, B18 7QH, UK

SOURCE: Journal of Antimicrobial Chemotherapy (1992),

29(6), 649-60

CODEN: JACHDX; ISSN: 0305-7453

DOCUMENT TYPE: Journal

LANGUAGE: English

GI English

HO<sub>2</sub>C N NMe

I, R=H
II, R=CH<sub>2</sub>F

AB The in vitro activity of two new quinolone antimicrobials, rufloxacin (I) and MF 961 (II), together with the desmethylated metabolite of rufloxacin (MF 922) were compared with other orally administered agents against 622 bacterial strains. Against

Enterobacteriaceae and Pseudomonas aeruginosa, I was generally active (MIC90 1-8 mg/L) with the exception of Klebsiella and Serratia spp. (MIC90 32 mg/L) and Enterobacter spp. (MIC90 64 mg/L). The respiratory pathogens Haemophilus influenzae and Moraxella catarrhalis were susceptible to I (MIC90 0.5 and 1 mg/L, resp.), but Streptococcus pneumoniae was less susceptible (MIC90 32 Staphylococcus aureus was susceptible to I (MIC90 2 mg/L). The I metabolite, MF 922, was generally as active as its parent. II was usually 2-fold more active than I. All 3 compds. were 4-16 times less active than norfloxacin, but I was as active or somewhat more active than norfloxacin against Staphylococcus spp. Any strains showing decreased susceptibility to other quinolones exhibited cross resistance to these new agents. The MBC of I and MF 922 was within one diln. of the MIC, and human serum had little effect upon the activity of both agents. The protein binding of I and MF 922 at 1 and 10 mg/L was 55 and 63.8% and 30.3% and 32.6%, resp. The activity of rufloxacin against four strains of Chlamydia trachomatis and one strain of Chlamydia pneumoniae was The MIC for C. trachomatis was 4-8 mg/L and 4 mg/L for C. pneumoniae.

L5 ANSWER 10 OF 21 MEDLINE

ACCESSION NUMBER: 92115389 MEDLINE

DOCUMENT NUMBER: 92115389 PubMed ID: 1766717

TITLE: Chlamydia pneumoniae (TWAR) in neonates.

AUTHOR: Matthews R S; Mohite A; Addy D P; Wise R

SOURCE: PEDIATRIC INFECTIOUS DISEASE JOURNAL, (1991 Dec) 10

(12) 956-7.

Journal code: 8701858. ISSN: 0891-3668.

PUB. COUNTRY: United States

DOCUMENT TYPE: Letter LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 199202

ENTRY DATE: Entered STN: 19920308

Last Updated on STN: 19920308 Entered Medline: 19920214

L5 ANSWER 11 OF 21 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.

DUPLICATE 5

ACCESSION NUMBER: 1991:226713 BIOSIS

DOCUMENT NUMBER: BA91:118173

TITLE: ISOLATION CLONING MAPPING AND NUCLEOTIDE SEQUENCING OF THE GENE ENCODING FLAVODOXIN IN ESCHERICHIA-COLI.

AUTHOR(S): OSBORNE C; CHEN L-M; MATTHEWS R G

CORPORATE SOURCE: DEP. BIOL. CHEM., UNIV. MICHIGAN, ANN ARBOR, MICH.

8109.

SOURCE: J BACTERIOL, (1991) 173 (5), 1729-1737.

CODEN: JOBAAY. ISSN: 0021-9193.

FILE SEGMENT: BA; OLD LANGUAGE: English

AB The flavodoxins constitute a highly conserved family of small, acidic electron transfer proteins with flavin mononucleotide prosthetic groups. They are found in prokaryotes and in red and green algae, where they provide electron at low potentials for the reduction of nitrogen by nitrogenase, for the light-dependent reduction of NADP+ in photosynthesis, and for the reduction of sulfite. Proteins with the physical characteristics of flavodoxins

have been implicated in the reductive activation of pyruvate formate-lyase and cobalamin-dependent methionine synthase in Escherichia coli. We have purified flavodoxin to homogeneity from E. coli, determined its N-terminal amino acid sequence, and used this sequence to construct a 64-fold degenerate oligonucleotide probe for the flavodoxin gene. Because the phenotype of a flavodoxin mutant is not known, we used this degenerate probe to screen the phages of Kohara library and identified two phages, with inserts mapping at .apprx. 16 min, that hybridized to the probe. The flavodoxin gene, designated fldA, was subcloned from the DNA in the overlap region of these two clones. The deduced amino acid sequence, determined by nucleotide sequencing of the flavodoxin gene, shows strong homology with flavodoxins from nitrogen-fixing bacteria and cyanobacteria. The fldA gene maps at 15.9 min on the E. coli chromosome and is transcribed in a counterclockwise direction.

L5 ANSWER 12 OF 21 EMBASE COPYRIGHT 2003 ELSEVIER SCI. B.V.DUPLICATE

6

ACCESSION NUMBER: 92041225 EMBASE

DOCUMENT NUMBER: 1992041225

TITLE: Chlamydia pneumoniae (TWAR) in neonates

[1].

AUTHOR: Matthews R.S.; Mohite A.; Addy D.P.; Wise

R.

CORPORATE SOURCE: Dudley Road Hospital, Birmingham, United Kingdom

SOURCE: Pediatric Infectious Disease Journal, (1991) 10/12

(956-957).

ISSN: 0891-3668 CODEN: PIDJEV

COUNTRY: United States

DOCUMENT TYPE: Journal; Letter

FILE SEGMENT: 004 Microbiology

007 Pediatrics and Pediatric Surgery

030 Pharmacology

037 Drug Literature Index

LANGUAGE: English

L5 ANSWER 13 OF 21 HCAPLUS COPYRIGHT 2003 ACS DUPLICATE 7

ACCESSION NUMBER: 1991:651968 HCAPLUS

DOCUMENT NUMBER: 115:251968

TITLE: In-vitro susceptibility of Chlamydia pneumoniae (TWAR) to seven antibiotics

AUTHOR(S): Cooper, M. A.; Baldwin, D.; Matthews, R.

S.; Andrews, J. M.; Wise, R.

CORPORATE SOURCE: Dep. Microbiol., Dudley Road Hosp., Birmingham,

UK

SOURCE: Journal of Antimicrobial Chemotherapy (1991),

28(3), 407-13

CODEN: JACHDX; ISSN: 0305-7453

DOCUMENT TYPE: Journal LANGUAGE: English

AB A modification of an immunofluorescence method previously used to study the in vitro antimicrobial susceptibilities of C. trachomatis was used to investigate the activity of seven antimicrobials against a strain of C. pneumoniae. Adding antimicrobial to preinfected cells gave higher MICs (min. inhibitory concns.) and MLCs (min. lethal concns.) than when cells were infected in the presence of the antimicrobials, and this difference in methodol. could account for the discrepancy between these results and those of

others. Of the antimicrobials studied, clarithromycin and its 14-hydroxy metabolite were the most active agents; sparfloxacin was more active than ciprofloxacin, but no more active than more conventional antichlamydial agents.

L5 ANSWER 14 OF 21 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 1991:535104 BIOSIS

DOCUMENT NUMBER: BR41:124839

TITLE: THE ACTIVITY OF SPARFLOXACIN AND OTHER AGENTS AGAINST

CHLAMYDIA-PNEUMONIAE THE EFFECT OF PRE AND .

POST ANTIBIOTIC EXPOSURE.

AUTHOR(S): WISE R; ANDREWS J M; COOPER M A; MATTHEWS R

CORPORATE SOURCE: DUDLEY ROAD HOSP., BIRMINGHAM B18 7QH, UK.

SOURCE: THIRTY-FIRST INTERSCIENCE CONFERENCE ON ANTIMICROBIAL

AGENTS AND CHEMOTHERAPY, CHICAGO, ILLINOIS, USA, SEPTEMBER 29-OCTOBER 2, 1991. PROGRAM ABSTR, (1991)

31 (0), 212. CODEN: POCHES.

DOCUMENT TYPE: Conference FILE SEGMENT: BR; OLD LANGUAGE: English

L5 ANSWER 15 OF 21 MEDLINE DUPLICATE 8

ACCESSION NUMBER: 91324522 MEDLINE

DOCUMENT NUMBER: 91324522 PubMed ID: 1907617

TITLE: Immunoblotting and culture positive endocarditis.

AUTHOR: Clark I; Burnie J P

CORPORATE SOURCE: Department of Medical Microbiology, University of

Manchester Medical School.

SOURCE: JOURNAL OF CLINICAL PATHOLOGY, (1991 Feb) 44 (2)

152-6.

Journal code: 0376601. ISSN: 0021-9746.

PUB. COUNTRY: ENGLAND: United Kingdom

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Abridged Index Medicus Journals; Priority Journals

ENTRY MONTH: 199109

ENTRY DATE: Entered STN: 19910929

Last Updated on STN: 19910929 Entered Medline: 19910909

AB Serum samples from patients with endocarditis due to Streptococcus mutans, Streptococcus pneumoniae, Streptococcus agalactiae, Streptococcus lactis and a "nutritionally" variant streptococcus were immunoblotted against antigenic extracts from all five species. In S mutans endocarditis there was an endocarditis specific pattern of IgM against bands of 220, 200, and 190 kilodaltons. In S pneumoniae IgM against antibody of a molecular weight greater than 150 kilodaltons was specific to endocarditis. In S agalactiae IgM against bands at 82, 71, and 66-67 kilodaltons was endocarditis specific. In S lactis endocarditis specific IgM was present against antigenic bands at 105, 66, 61 and 58 kilodaltons. With the "nutritionally" variant streptococcus it was impossible to distinguish between cases of endocarditis and

L5 ANSWER 16 OF 21 HCAPLUS COPYRIGHT 2003 ACS DUPLICATE 9

ACCESSION NUMBER: 1991:58770 HCAPLUS

DOCUMENT NUMBER: 114:58770

controls.

TITLE: In vitro activity of sparfloxacin, a new

quinolone antimicrobial agent

AUTHOR(S): Cooper, M. A.; Andrews, J. M.; Ashby, J. P.;

Matthews, R. S.; Wise, R.

CORPORATE SOURCE: Dep. Microbiol., Dudley Road Hosp., Birmingham,

UK

SOURCE: Journal of Antimicrobial Chemotherapy (1990),

26(5), 667-76

CODEN: JACHDX; ISSN: 0305-7453

DOCUMENT TYPE: Journal LANGUAGE: English

The in vitro activity of sparfloxacin (AT-4140), a new difluorinated AB quinolone, was compared with those of ciprofloxacin, temafloxacin, and selected members of other groups of antimicrobial agents, against 651 recent distinct clin. isolates and strains with known mechanisms of resistance. Three strains of Chlamydia trachomatis were also studied. The MICs for 90% of the Enterobacteriaceae were 0.06-1 mg/L; for Pseudomonas aeruginosa the MIC90 was 2 mg/L. Sparfloxacin was 16-fold more active against Acinetobacter spp. than ciprofloxacin. For Staphylococcus spp., Streptococcus spp., and Enterococcus faecalis, the MIC90 was 0.25-1 mg/L; sparfloxacin was 4-fold more active against Streptococcus pneumoniae than ciprofloxacin. Ninety percent of strains of Haemophilus influenzae, Branhamella catarrhalis, and Neisseria spp. were inhibited by <0.03 mg/L; for Bacteroides fragilis the MIC90 was 1 mg/L. The 3 strains of C. trachomatis were susceptible to 0.06-0.12 mg/L sparfloxacin, which was 16-fold more active than ciprofloxacin. There was cross resistance among the quinolones, but not between the quinolones and other groups of antimicrobials. The protein binding of sparfloxacin was 40% and serum had little effect on its activity.

L5 ANSWER 17 OF 21 HCAPLUS COPYRIGHT 2003 ACS DUPLICATE 10

ACCESSION NUMBER: 1988:435176 HCAPLUS

DOCUMENT NUMBER: 109:35176

TITLE: In vitro activity of lomefloxacin, a new

quinolone antimicrobial agent, in comparison

with those for other agents

AUTHOR(S): Wise, R.; Andrews, J. M.; Ashby, J. P.;

Matthews, R. S.

CORPORATE SOURCE: Dep. Med. Microbiol., Dudley Road Hosp.,

Birmingham, B18 7QH, UK

SOURCE: Antimicrobial Agents and Chemotherapy (1988),

32(5), 617-22

CODEN: AMACCO; ISSN: 0066-4804

DOCUMENT TYPE: Journal LANGUAGE: English

AB The in vitro activity of lomefloxacin (I), a new difluorinated quinolone, was compared with those of ofloxacin, ciprofloxacin, fleroxacin, amoxicillin, cefuroxime, and trimethoprim against 585 recent clin. isolates and other strains with known mechanisms of resistance. The MICs of I against 90% of the members of the family Enterobacteriaceae, Pseudomonas aeruginosa, and staphylococci were between 0.25 and 4 .mu.g/mL. Ninety percent of Neisseria sp. and Haemophilus influenzae were susceptible to .ltoreq.0.06 .mu.g/mL, and streptococci (including S. pyogenes, S. pneumoniae, and enterococci) and Bacteroides feragilis were susceptible to 8 .mu.g/mL. I was comparable in activity to fleroxacin and ofloxacin, but it was less active than ciprofloxacin. There was

cross-resistance between the quinolone group of antimicrobial agents. The protein binding of I was 15.4%, and serum had little effect on the activity of the compd. However, urine at pH 5.0 decreased the activity by 2-8-fold compared with that at pH 7.0.

ANSWER 18 OF 21 EMBASE COPYRIGHT 2003 ELSEVIER SCI. B.V.

88049469 EMBASE ACCESSION NUMBER:

DOCUMENT NUMBER: 1988049469

TITLE: Chlamydial rhinitis neonatorum.

Kent S.E.; Matthews R.S. AUTHOR:

CORPORATE SOURCE: Birmingham Children's Hospital, Ladywood, Birmingham

B16 8ET, United Kingdom

Journal of Laryngology and Otology, (1987) 101/11 SOURCE:

ISSN: 0022-2151 CODEN: JLOTAX

(1193-1197).

COUNTRY: United Kingdom

DOCUMENT TYPE: Journal

FILE SEGMENT: 004 Microbiology

> Pediatrics and Pediatric Surgery 007

010 Obstetrics and Gynecology

011 Otorhinolaryngology

LANGUAGE: English SUMMARY LANGUAGE: English

This paper reports the case of a five-week-old child who developed severe rhinitis with epistaxes, due to infection with chlamydia trachomatis. The infection was acquired from the mother's genital tract during birth but the true diagnosis was not suspected for some time. Chlamydia trachomatis is well recognized as one of the causes of neonatal conjunctivitis and pneumonia. However, its presence in the upper respiratory tract is thought usually to be asymptomatic (Oriel and Ridgway, 1982). Little attention has been focused on its role in neonatal rhinitis. This paper draws to the otolaryngologist's attention the entity of chlamydial rhinitis neonatorum and discusses the epidemiology, diagnosis and management of the condition.

ANSWER 19 OF 21 EMBASE COPYRIGHT 2003 ELSEVIER SCI. B.V.

ACCESSION NUMBER: 85172703 EMBASE

DOCUMENT NUMBER: 1985172703 TITLE: CM-40874.

Burnie J.; Matthews R. AUTHOR:

CORPORATE SOURCE: United Kingdom

Drugs of the Future, (1985) 10/3 (193-195). SOURCE:

CODEN: DRFUD4

COUNTRY: Spain DOCUMENT TYPE: Journal

FILE SEGMENT: 037 Drug Literature Index

> 052 Toxicology

LANGUAGE: English

ANSWER 20 OF 21 MEDLINE

78198713 MEDLINE ACCESSION NUMBER:

DOCUMENT NUMBER: 78198713 PubMed ID: 78425 TITLE: Multiply resistant pneumococcus.

AUTHOR: Meers P D; Matthews R B

LANCET, (1978 Jul 22) 2 (8082) 219. SOURCE:

Journal code: 2985213R. ISSN: 0140-6736.

PUB. COUNTRY: ENGLAND: United Kingdom

> 308-4994 Searcher : Shears

DOCUMENT TYPE:

Letter

LANGUAGE:

English

FILE SEGMENT:

Abridged Index Medicus Journals; Priority Journals

ENTRY MONTH:

197809

ENTRY DATE:

Entered STN: 19900314

Last Updated on STN: 19950206 Entered Medline: 19780901

ANSWER 21 OF 21 EMBASE COPYRIGHT 2003 ELSEVIER SCI. B.V.

ACCESSION NUMBER:

78377563 EMBASE

DOCUMENT NUMBER:

1978377563

TITLE:

Multiply resistant pneumococcus.

AUTHOR:

Meers P.D.; Matthews R.B.

CORPORATE SOURCE:

Publ. Hlth Lab., Gen. Hosp., Plymouth PL4 8NN, United

Kingdom

SOURCE:

Lancet, (1978) 2/8081 (155-156).

CODEN: LANCAO United Kingdom

COUNTRY:

Journal

DOCUMENT TYPE: FILE SEGMENT:

037 Drug Literature Index Microbiology

004

English

LANGUAGE: A pneumococcus resistant to chloramphenicol, tetracycline and penicillin was isolated from a holidaymaker from Spain, who was admitted to hospital in Plymouth with an acute skin condition. She had a productive cough, and from mucopurulent sputum a pneumococcus (type 23, Danish nomenclature) was isolated. On routine testing this was found to be resistant to choramphenical and tetracycline, and the zone of inhibition round the penicillin disc (1.5 units) was reduced from the expected .gtoreg.10 mm to 7 mm, measured radially from the edge of the disc. By the agar dilution method, using a minimal-growth endpoint, the minimum inhibitory concentration (M.I.C.) of penicillin was 0.25 .mu.g/ml compared with an M.I.C. of 0.03 .mu.g/ml for a sensitive strain. The M.I.C.s of tetracycline and chloramphenical were both 20 .mu.g/ml. The inoculum used in these tests was about 106 organisms.

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                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION UMBER: JP 224711/94
FILING DATE: 20-SEP-1994
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APPLICATION NUMBER: JP 106008/95
FILING DATE: 28-APR-1995
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1155 Avenue of the Americas
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CHLANYDIA PNEUMONIAE ANTIGENIC POLYPEPTIDES,
CHEREFOR, RECOMBINANT VECTORS CARRYING THE DNAS, TRANSFORMANTS
CONTAINING THE RECOMBINANT VECTORS, METHOD FOR PRODUCTION OF
ANTIBODY, METHOD AND REAGRENTS FOR DETECTION AND/OR MEASUREMENT
OF ANTIBODY, METHOD AND AGENTS FOR DIAGNOSIS OF CHLAMYDIA
PNEUMONIAE INFECTIONS, PROBES AND PRIMERS FOR DETECTION AND/OR
MEASUREMENT OF CHLAMYDIA PNEUMONIAE GENE, AND METHOD AND
REAGENTS FOR DETECTION AND/OR MEASUREMENT OF CHLAMYDIA
PNEUMONIAE GENE
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RESULT 2 US-08-809-326A-15

Sequence 15, Application US/08809326A Patent No. 6165478 GENERAL INFORMATION: APPLICANT: Izutsu, Hiroshi APPLICANT: Obara, Kazuhiko

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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUIENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
APPLICATION UNMBER: JP 106
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
APPLICATION UNMBER: JP 106
FILING DATE: 28-APR-1995
ATTORNEY/AGENT INFORMATION:
ANAME. APPLICATION:
ANAME. APPLICATION
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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

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5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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Copyright (c) 1993 - 2003 Compugen
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RESULT 1
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                                                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatibl
OPERATING SYSTEM: PC COS,
SOFTWARE: Patentin Release
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
FILING DATE: 19-MAR-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: IZUUSU, HIPSHI
APPLICANT: IZUUSU, HIPSHI
APPLICANT: Obara, Kazuhiko
APPLICANT: Matsumoto, Akira
TITLE OF INVENTION: CHLANYDI;
TITLE OF INVENTION: THEREFOR,
TITLE OF INVENTION: OF ANTIHODY,
TITLE OF INVENTION: OF ANTIHODY,
TITLE OF INVENTION: OF ANTIHODY,
TITLE OF INVENTION: PNEUMONII
TITLE OF INVENTION: MEASUREMH
TITLE OF INVENTION: REAGENTS
TITLE OF INVENTION: PNEUMONII
TODERSCONDIENCES: 31
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STATE: New York
COUNTRY: USA
ZIP: Jan
            PRIOR APPLICATION NUMBER: JP 106006/95
APPLICATION DATA:
APPLICATION NUMBER: JP 7077
FILING DATE: 70777
                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2/
FILLING DATE: 20-SEP-1994
PRIOR APPLICATION DATA:
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ADDRESSEE: Pennie &
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1155 Avenue of the Americas
                                                                                                                                                                                                                         NUMBER: US/08/809,326A
19-MAR-1997
                                                                                                                                                                                                                                                                                                            Compatible
PC-DOS/MS-DOS
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TUSED PROTEINS CONTAINING THE POLYPEPTIDES, DNAS CODING
THEREFOR, RECOMBINANT VECTORS CARRYING THE DNAS, TRANSFORMANTS
CONTAINING THE RECOMBINANT VECTORS, METHOD FOR PRODUCTION OF
ANTIBODY, METHOD AND REAGENTS FOR DETECTION AND/OR MEASUREMENT
OF ANTIBODY, METHOD AND AGENTS FOR DIAGNOSIS OF CHLAMYDIA
PNEUMONIAE INFECTIONS, PROBES AND PRIMERS FOR DETECTION AND/OR
MEASUREMENT OF CHLAMYDIA PNEUMONIAE GENE, AND METHOD AND
REAGENTS FOR DETECTION AND/OR MEASUREMENT OF CHLAMYDIA PNEUMONIAE GENE, AND METHOD AND
REAGENTS FOR DETECTION AND/OR MEASUREMENT OF CHLAMYDIA
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US-08-348-891A-2
US-08-351-224E-8
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US-08-451-526-49
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US-09-311-574-2
US-09-311-574-3
US-09-381-224E-3
US-09-381-224E-3
US-08-484-494-2
US-08-484-494-2
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Sequence 15, Application US/08809326A Patent No. 6165478
GENERAL INFORMATION:
APPLICANT: Izutsu, Hiroshi
APPLICANT: Obara, Kazuhiko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: US-08-809-326A-1
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TELEPHONE: (212) 869-8864/
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 488 amino acids
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Best Local :
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FILING DATE: 28-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Miller Charles E.
REGISTRATION NUMBER: 24,57
REFERENCE/DOCKET NUMBER: 7
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APPLICATION NUMBER: JP
FILING DATE: 28-APR-19
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JF
FILING DATE: 28-APR-19
PRIOR APPLICATION DATA:
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TOPOLOGY: line-
MOLECUTY
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487; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: JP 1
FILING DATE: 28-APR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 224711/94
FILING DATE: 20-SEP-1994
PRIOR APPLICATION DATA:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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ADDRESSEE: Pennie & Edmonds LLP
                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
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                                                              162
   222
                                                                                                                                                                                                                                                                                                                                                        NAME: Miller, Charles E.
REGISTRATION NUMBER: 24,576
REFERENCE/DOCKET NUMBER: 7426-043-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: JP 106008/95 FILING DATE: 28-APR-1995
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487; Conserv
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10036-2711
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Pred. No. 0;
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US-08-809-326A-5
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GENERAL INFORMATION:
                                                                                                                                                                                  COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, VE
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,326A
FILING DATE: 19-MAR-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICANT: Matsumoto,
                      FILING DATE: 28-APR-PRIOR APPLICATION DATA:
                                                                PRIOR APPLICATION DATA:
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                                                                                                                 APPLICATION NUMBER: JP 2: FILING DATE: 20-SEP-1994
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ZIP: 10036-2711
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                                               28-APR-1995
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FUSED PROTEINS CONTAINING THE POLYPEPTIDES,
THEREFOR, RECOMBINANT VECTORS CARRYING THE DNAS, TRANSFORMA
CONTAINING THE RECOMBINANT VECTORS, METHOD FOR PRODUCTION O
ANTIBODY, METHOD AND REAGENTS FOR DETECTION AND/OR MEASUREM
OF ANTIBODY, METHOD AND AGENTS FOR DIAGNOSTS OF CHLAMYDIA
PNEUMONIAE INFECTIONS, PROBES AND PRIMERS FOR DETECTION AND
MEASUREMENT OF CHLAMYDIA PNEUMONIAE GENE, AND METHOD AND
REAGENTS FOR DETECTION AND/OR MEASUREMENT OF CHLAMYDIA
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of the Amer
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                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 259 amino acids
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APPLICANT:
                                CORRESPONDENCE ADDRESS
                                                      NUMBER OF SEQUENCES:
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FILING DATE: 28-APR-1995
ATTORNEY/AGENT INFORMATION:
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TELEFAX: (212) 869-8864/9741
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REFERENCE/DOCKET NUMBER: 7426-043-999
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Matsumoto, Akira
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             Pennie & Edmonds LLP
Avenue of the Americas
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28-APR-1995
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28-APR-1995
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                                                                                                  CHLAMYDIA PNEUMONIAE ANTIGENIC POLYPEPTIDES,
FUSED PROTEINS CONTAINING THE POLYPEPTIDES,
THEREFOR, RECOMBLIANIT VECTORS CARRYING THE DNAS, TRANSFORMANTS
CONTAINING THE RECOMBINANT VECTORS, METHOD FOR PRODUCTION OF
ANTIBODY, METHOD AND REAGENTS FOR DETECTION AND/OR MEASUREMENT
OF ANTIBODY, METHOD AND AGENTS FOR DIAGNOSIS OF CHLAMYDIA
PNEUMONIAE INFECTIONS, PROBES AND PRIMERS FOR DETECTION AND/OR
MEASUREMENT OF CHLAMYDIA PNEUMONIAE GENE, AND METHOD AND
MEASUREMENT OF CHLAMYDIA PNEUMONIAE GENE, AND METHOD AND
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100.0%; F1
                                                                       PNEUMONIAE
                                                                                          REAGENTS
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Pred. No. 1.5e-226;
                                                                     FOR DETECTION AND/OR MEASUREMENT OF CHLAMYDIA AE GENE
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; MOLECULE TYPE: peptide US-08-809-326A-2
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: JP 106
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 106
FILING DATE: 28-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: MILLEY CHARLES E
REGISTRATION NUMBER: 24.57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 106009/95
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
TO 106010/95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 74: TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: JP 106006/95
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
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241
                               244 QKSKDLEGTMDTVNTVMIA 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                     EIGLALAKAIQTLGEATKSALSNYASTQAQADQTNKLGLEKQAIKIDKEREEYQEMKAAE
                                                                                                                                                               EEASKSMESTLESLQSLSAAQMKEVEAVVVAALSGKSSGSAKLETPELPKPGVTPRSEVI 183
                                                                                                                                                                                                                                       ASGKDKTSSTTKTETAPQQGVAAGKESSESQKAGADTGVSGAAATTASNTATKIAMQTSI 123
                                                                                                                                           EEASKSMESTLESLQSLSAAQMKEVEAVVVAALSGKSSGSAKLETPELPKPGVTPRSEVI 180
                                                                                                                                                                                                                 ASGKDKTSSTTKTETAPQQGVAAGKESSESQKAGADTGVSGAAATTASNTATKIAMQTSI 120
                                                                    EIGLALAKAIQTLGEATKSALSNYASTQAQADQTNKLGLEKQAIKIDKEREEYQEMKAAE
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10036-2711
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(212) 869-8864/9741
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19-MAR-1997
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100.0%; Pred. No. 1.6e-226;
tive 0; Mismatches 0;
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                                                                            Query Match
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                                                                                                                                                                                                       TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
                                                                                                                                    MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                          NAME: Miller, Charles E. REGISTRATION NUMBER: 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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                                                                                                                                                                                     LENGTH:
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                                                            Local
4 MSISSSSGPDNQKNIMSQVLTSTPQGVPQQDKLSGNETKQIQQTRQGKNTEMESDATIAG 63
                                                          Similarity
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10036-2711
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                                                                                                                                                                                                                                                                 (212) 869-8864/9741
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                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PatentIn Release #1.0,
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                                                                                                                                                        linear
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                                                        52.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHLAMIDIA PNEUMONIAE ANTIGENIC POLYPEPTIDES,
PROTEINS CONTAINING THE POLYPEPTIDES, DNAS CODING
PRESED PROTEINS CONTAINING THE POLYPEPTIDES, DNAS CODING
THEREFOR, RECOMBINANT VECTORS CARRYING THE DNAS, TRANSFORMANTS
CONTAINING THE RECOMBINANT VECTORS, METHOD FOR PRODUCTION OF
ANTIBODY, METHOD AND REAGENTS FOR DETECTION AND/OR MEASUREMENT
OF ANTIBODY, METHOD AND AGENTS FOR DIAGNOSTS OF CHLAMYDIA
PREDUMONIAE INPECTIONS, PRODES AND PRIMERS FOR DETECTION AND/OR
MEASUREMENT OF CHLAMYDIA PNEUMONIAE GENE, AND METHOD AND
REAGENTS FOR DETECTION AND/OR MEASUREMENT OF CHLAMYDIA
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                                 Score 259; DB 4; ...; Pred. No. 2.5e-226; Pred. No. 2.5e-226;
                                                                                                                                                                                                                                                                                                                          7426-043-999
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LENGTH: 27
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APPLICANT: Ranum et al.

TITLE OF INVENTION: SCA7 GENE AND METHODS OF FILE REFERENCE: University of Minnesota CURRENT APPLICATION NUMBER: US/09/135,994A CURRENT FILING DATE: 1998-08-18

EARLIER APPLICATION NUMBER: 60/056,170

EARLIER APPLICATION NUMBER: 60/056,170

EARLIER FILING DATE: 1997-08-19

NUMBER OF SEQ ID NOS: 14

NUMBER OF SEQ ID NOS: 14
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                                                                                                                                                                                                                           APPLICANT: Hinman, Michael B.
TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK
TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL
TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF
NUMBER OF SEQUENCES: 69
                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                     APPLICANT: Lewis, RAPPLICANT: Xu, Ming APPLICANT: Hinman,
                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              402
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                                                                                                                                                 ADDRESSEE: Birch, Stewart, Kolasch & Birch STREET: 301 No. 5728810th Washington Street CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17
                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                              COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EIGLALAKAIQTLGEATKSALSNYASTQAQADQTNKLGLEKQAIKIDKEREEYQEMKAAE 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAAAGGAA 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QKSKDLEGTMDTVNTVMIA 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EEASKSMESTLESLQSLSAAQMKEVEAVVVAALSGKSSGSAKLETPELPKPGVTPRSEVI 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ASGKDKTSSTTKTETAPQQGVAAGKESSESQKAGADTGVSGAAATTASNTATKIAMQTSI 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EIGLALAKAIQTLGEATKSALSNYASTQAQADQTNKLGLEKQAIKIDKEREEYQEMKAAE 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EEASKSMESTLESLQSLSAAQMKEVEAVVVAALSGKSSGSAKLETPELPKPGVTPRSEVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ASGKDKTSSTTKTETAPQQGVAAGKESSESQKAGADTGVSGAAATTASNTATKIAMQTSI 123
                                                                                                                                                                                                                                                                                                                                                                               50, Application US/08425069
5. 5728810
                                                                                                                                                                                                                                                                                                                                                             INFORMATION:
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8; Conser
                                                                                                 22046
                                                                                                                Virginia
Y: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                        Randolph V.
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   Version #1
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RESULT 8
US-08-317-844B-50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MUIPHY JI., Gerald M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1447
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 241-1300
TELEFAX: (703) 241-2848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: XU, Ming
APPLICANT: XU, Ming
APPLICANT: Hinman, Michael B.
APPLICANT: Hinman, Michael B.
TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK
TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF
TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF
TITLE OF SEQUENCES: 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 50: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: 301 No. 5989894th Washington Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1447-106P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
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ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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12 GAAAAGGA 19
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                                                                                                                                                APPLICATION NUMBER: US/0
FILING DATE: 04-OCT-1994
                                                                                                                                                                                                                                                                                                                                 STATE: Virginia
                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                      CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: /label= silkl_repeat
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TYPE: amino acid
STRANE amino acid
STRANE amino acid
STRANE amino acid
TOTALE Amino acids
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                                                                                                                                                                                                                                                                                                  22046
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100.0%; Fred. No.
14 ve 0; Mismatches
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                                                         1447-105P
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5. 2.7;
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Query Match
Best Local Similarity
"hes 8; Conserv
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; LOCATION: 1..28
; OTHER INFORMATION:
US-08-317-844B-50
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APPLICANT: Lewis, I
APPLICANT: Xu, Min
APPLICANT: Hinman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 61, Application US/08425069 Patent No. 5728810
                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,069
EILING DATE: 19-APR-1995
CLASSIFICATION: 435
                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 248345
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 22046
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                TOPOLOGY: not relevant MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M
REGISTRATION NUMBER: 28,97
FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hinman, Michael B.

TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK

TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL

TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: nephila clavipes FEATURE:
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                                                                                LENGTH: 30 amino acids
TYPE: amino acid
STRANDENESS: not rele
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: no
TOPOLOGY: not re
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Y: U.S.A.
                                                                                                                                                                                                 (703) 205-8050
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Xu, Ming
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                 internal
                                                                                      not relevant
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100.0%; Pred. No. 2.
ive 0; Mismatches
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                                                                                                                                                                                                                                                                    28,977
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                                                                                                                                                                                                                                                     1447-106P
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o. 2.7;
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US-08-317-844B-61
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                              Query Match
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   Matches
                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: MUTPHY Jr., Gerald M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1447
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 241-1300
TELEPAX: (703) 241-2848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                           NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: 301 No. 5989894th Washington Street
                                                                                                                        FEATURE:
                                                                                                                                                    FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                 MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: FEATURE:
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TELEFAX: 248345
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/0 FILING DATE: 04-OCT-1994 CLASSIFICATION: 435
                                                                                          NAME/KEY:
                                                                                                                                     ORGANISM:
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les 8; Conserv
   Local Similarity es 8; Conserv
                                                                            OTHER INFORMATION:
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   Conservative
                                                                                                                                      nephila clavipes
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1..30
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1..30
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PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL
CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF
1.6%; Score 8; 1
100.0%; Pred. No.
tive 0; Mismatcl
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                                                                                                                                                                                                                                                                                           61:
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 Mismatches
              DB 2;
o. 2.9;
                              Length 30;
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Indels
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Gaps
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RESULT 12
US-08-317-844B-6
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              Sequence 6, Application US/08317844B Patent No. 5989894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6
Patent No.
                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 8; Conserv
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/425

FILING DATE: 19-APR-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: MUTPINY JT., Gerald M

REGISTRATION NUMBER: 28,97

REFERENCE/DOCKET NUMBER: 1447

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION: APPLICANT: Lewis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hinman, Michael B.
TITLE OF INVENTION: ISOLATED
TITLE OF INVENTION: PROTEIN,
TITLE OF INVENTION: CONTAININ
NUMBER OF SEQUENCES: 69
                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide FRAGMENT TYPE: internal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                        OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                      293 GAAAAGGA 300
                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: 301 No. 5728810th Washington Street
CITY: Falls Church
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 GAAAAGGA 19
                                                                                                                    6 GAAAAGGA 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33 amino acids
                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                               Peptide
1..33
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Xu, Ming
                                                                                                                                                                                                                                                                                                                                                                                              Nephila clavipes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (703)
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PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL
CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF
: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       205-8000
                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                        /label= representative /note= "This peptide is a representative one that illustrates the gygyg hexamer repeat motif of the spider silk protein I."
                                                                                                                                                                                                     1.6%; Score 8;
100.0%; Pred. No.
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                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                   Length 33;
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                                                                                                                                                                                       Indels
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RESULT 13
US-08-185-414E-2
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                                                                                                                                                                                                                        Sequence 2, Applic Patent No. 5556953
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 1.6%; Score 8; DB 2; Best Local Similarity 100.0%; Pred. No. 3.2; Matches 8; Conservative 0; Mismatches
                                                                                       GENERAL INFORMATION:
APPLICANT: Zhang, Lei
APPLICANT: Vijay, Hari M.
APPLICANT: Rode, Harold
TITLE OF INVENTION: ALLERGEN OF CLADOSPORIUM HERBARUM
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIT
TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR
TITLE OF INVENTION: CONTAINING THE ISOLATED DNA,
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: 301 No. 5989894th Washington Street
CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (703) 241-284
TELEX: 248345
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: MUTPHY JT., Gerald M
REGISTRATION UNMBER: 28,977
REFERENCE/DOCKET NUMBER: 1447
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 241-1300
TELEPEX: (703) 241-2848
                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide FRAGMENT TYPE: internal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                        293 GAAAAGGA 300
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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        ADDRESSEE: George A. Seaby
ADDRESSEE: Seaby and Maclean
STREET: 880 Wellington Street, Suite 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                     6 GAAAAGGA 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Nephila clavipes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/317,844B
FILING DATE: 04-OCT-1994
CLASSIFICATION: 435
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Ottawa
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GY: linear
                                                                                                                                                                                                                                          Application US/08185414E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lewis, Randolph V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xu, Ming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ISOLATED DNA CODING FOR SPIDER SILK
PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL
CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= representative /note= "This peptide is a representative one that illustrates the ggxgyg hexamer repeat motif of the spider silk protein I."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 33;
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RESULT 15
US-08-911-319A-1
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Best Local Similarity
Themes 8; Conserv.
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                                                                                         Qy
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US-09-135-994-12
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                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12
LENGTH: 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12, Application US/09135994A Patent No. 6280938
                                                                                                                                                                                                                                                                                 APPLICANY: RANUM et al.

TITLE OF INVENTION: SCA7 GENE AND METHODS OF USE
FILE REFERENCE: University of Minnesota
CURRENT APPLICATION NUMBER: US/09/135,994A
CURRENT FILING DATE: 1998-08-18
EARLIER APPLICATION NUMBER: 60/056,170
EARLIER FILING DATE: 1997-08-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (613) 232-5831
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
GTEANDERUECS
                                                                                                                                                                                                                    TYPE: PRT
                                                                                         294 AAAAGGAA 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 17
TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 232-5815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/0:
FILING DATE: January 24,
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: George A. Seaby
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compate OPERATING SYSTEM: PC-DC SOFTWARE: ASCII Text CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: Canada
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
                                                               17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       293 GAAAAGGA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78 GAAAAGGA 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Ch2.1 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: George A. Sea REGISTRATION NUMBER:
                                                             AAAAGGAA 24
                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1..111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        January 24, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seaby
                                                                                                              1.6%; Score 8; DB / 100.0%; Pred. No. 12. ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1747
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                                                                                                                                                DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
5. 11;
                                                                                                                                                Length 129;
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                                                                                                                 Gaps
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Sequence 1, Application US/08911319A
Patent No. 5968798
GENERAL INFORMATION:

APPLICANT:

INFORMATION: CANT: Hillman,

Jennifer L.

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RESULT 16
US-09-352-619-1
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                                                                                                                                                                                                                                                                                                      Patent No. 6084070
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Hillman, Jennif
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMMEDIATE SOURCE:
LIBRARY: THP1NOT03
CLONE: 2447829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/911,319A FILING DATE: AUGUST 14, 1997 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                             TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Corley, Neil C
APPLICANT: Shah, Purvi
                                                                                                                                                                                                                                                                                                                                                                                                                            299 GAAGAAAA 306
                                       COMPUTER: IBM CONTROL OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                              29 GAAGAAAA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 1.6%; So Local Similarity 100.0%; Figs 8; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                STREET: 3174 POI
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Muenzen, Colette C. REGISTRATION NUMBER: 39,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
APPLICATION NUMBER:
                                                                         MEDIUM TYPE:
                                                                                                                     COUNTRY: USA
                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENGTH:
                                                                                                       94304
              ARE: FastSEQ for Windows Version 2.0 APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94304
                                                                                                                                     CA
                                                                                                                                                                                                                                                                                                                    Application US/09352619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Incyte Pharmaceuticals, Inc. 3174 Porter Dr.
                                                                                                                                                               3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          164 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                                        IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IBM Compatible
                                                                                                                                                                               Incyte Pharmaceuticals, Inc.
                                                                           Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                           HUMAN GLUTAREDOXIN BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HUMAN GLUTAREDOXIN BETA
                                                                                                                                                                                                                                                                       Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOS
 US/09/352,619
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US-08-775-009-37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 37 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                TELEFAX: (215) 568-34 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linea:
IMMEDIATE SOURCE:
LIBRARY: THP1NO:
CLONE: 2447829
                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DCS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/775,009
FILING DATE: 27-DEC-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: TRUSTILL DEVENOR VALUE

NAME: 
                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CH
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RECISTRATION NUMBER: 39,784
REFERENCE/DOCKET NUMBER: PF-0363 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
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NAME: Muenzen, Colette C.
REGISTRATION NUMBER: 39,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: No. 5935783el Genes Mapping in the Digeorge and TITLE OF INVENTION: Veliocardiofacial Syndrome Minimal Critical Region NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Gong, Weilong
APPLICANT: Emanuel, Beverly S.
APPLICANT: Budarf, Marcia L.
APPLICANT: Roe, Bruce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
PRIOR APPLICATION DATA:
MOLECULE TYPE:
                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    299 GAAGAAAA 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: One Liberty CITY: Philadelphia
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                                                                                                                                                                                                                                                                                                                                                             NAME: Trujillo, Doreen Yatko
REGISTRATION NUMBER: 35,719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz ADDRESSEE: No. 5935783ris, LLP STREET: One Liberty Place - 46th Floor
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                                                                                                                                                                                                                                                         TELEPHONE:
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                                          TOPOLOGY:
                                                                                                       LENGTH:
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5. 5935783
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                                                                     amino acid
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100.0%; Pred. No.
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US-08-775-009-37

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RESULT 19
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                                                                                     Sequence 3, Application US/08630552
Patent No. 5733314
GENERAL INFORMATION:
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US-08-364-081-3
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                                 APPLICANT: Ramesh K.
TITLE OF INVENTION: I
TITLE OF INVENTION: I
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (801)566-0750
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Alan J. Howarth
REGISTRATION NUMBER: 36,553
REFERENCE/DOCKET NUMBER: T71
TELECOMMUNICATION INFORMATION:
TELEPHONE: (801)566-6633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PATOR APPLICATION DATA:
APPLICATION NUMBER: 08/019,780
FILLING DATE: 19-FEB-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb storage COMPOTER: AST Advantage NB-SX20 OPERATING SYSTEM: DOS 6.2 SOFTWARE: Word Perfect 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Diskett
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260 GAAAAGGA 267
                                                                                                                                                                                                                                293 GAAAAGGA 300
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STATE: Utah
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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      ADDRESSEE:
                                                                                                                                                                                                                                                            Local Similarity
nes 8; Conserv
                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      294 AAAAGGAA 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U
ZIP: 84070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/364,081
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                                                                            Ramesh K. Prakash
                                                                                                                                                                                                                                                            Conservative
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Thorpe, No. 5723314th & Western
                    ADDRESS
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100.0%; Pr
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100.0%; pr
                                          Recombinant Antigen for Diagnosing Rheumatoid Arthritis
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Pred. No
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b; Pred. No. 19;
0; Mismatches
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o. 31;
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                                                                                                                                                                                                                                                                                   Length 331; `
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COMPUTER: IBM ThinkPad 340
OPERATING SYSTEM: DOS 6.2
SOFTWARE: WORD PERFECT 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16558
FILING DATE: 27-DEC-1994
CLASSIFICATION: DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/019,780
FILING DATE: 19-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Alan J. HOWARTH
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application PC/TUS9516558 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PILING DATE:
APPLICATION NUMBER: 08/019,78
FILING DATE: 19-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Alan J. Howarth
REGISTRATION NUMBER: 36,553
REFERENCE/DOCKET NUMBER: T781
TELECOMMUNICATION INFORMATION:
TELECPHONE: (801)566-6633
                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
MEDIUM TYPE: Storage
                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: AST Advant
                                                                                                                                                                                                                                                                 STREET: 9035
CITY: Sandy
STATE: Utah
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PRIOR APPLICATION NUMBER: 1
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                                                                                                                                                                                                                                       COUNTRY: U
                                                                                                                                                                                                                                                                                         ADDRESSEE: Thorpe, North & Western STREET: 9035 South 700 East, Suite 200
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CITY: Sandy
STATE: Utah
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nes 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
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ZIP: 84070
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                                                                                                                                                                                                                                                      USA
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SYSTEM: DOS 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Diskette, 3.5 inch,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.6%; Scc.
100.0%; Pr
                                                                                                                                                                                                                                                                                                                                               Recombinant Antigen for Diagnosing Rheumatoid Arthritis
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T781CIP
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31;
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REGISTRATION NUMBER:

36,553

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APPLICANT: Allen, Steve
APPLICANT: Lee, Jian Ming
TITLE OF INVENTION: Plant Protein Kinases
FILE REFERENCE: BB-1171
CURRENT APPLICATION NUMBER: US/09/347,801
CURRENT FILING DATE: 1999-07-02
EARLIER APPLICATION NUMBER: 60/092,438
EARLIER FILING DATE: July 10, 1998
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Microsoft Office 97
SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
"~+~hes 8; Conserv?
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US-08-556-978B-19
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; TYPE: PRT
; ORGANISM: Zea mays
US-09-347-801-18
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Best Local
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                COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD FOR WINDOWS 95
CURRENT APPLICATION DATA:
                                                                                                                                                                                   NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 331 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                           TITLE OF INVENTION: NOVEL RECOMBINANTLY PRODUCED TITLE OF INVENTION: SPIDER SILK ANALOGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                              APPLICANT:
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Local Similarity 100.0%; Pred. N
hes 8; Conservative 0; Misma
                                                                                                                                                                          CITY: WILMINTON
APPLICATION NUMBER: US/08/556,978B
                                                                                                                                         COUNTRY:
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                                                                                                                       19898
                                                                                                                                                         DELAWARE
                                                                                                                                       UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                              FAHNESTOCK, STEPHEN F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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(801)566-0750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.6%; Score 8; DB 100.0%; Pred. No. 58 tive 0; Mismatches
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Query Match
Best Local Similarity
"atches 8; Conserv."
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US-08-425-069-2
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Best Local Similarity
Thehes 8; Conserve
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                                                                                           Sequence 2, Application US/08425069 Patent No. 5728810 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Applic Patent No. 6280747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: PHILLIPPE, Michel
APPLICANT: GARSON, Jean-Claude
APPLICANT: ARRAUDERU, Jean-Pierre
APPLICANT: ARRAUDERU, Jean-Pierre
TITLE OF INVENTION: COSMETIC OR DERMATOLOGICAL COMPOSITION CONTACTING AT
TITLE OF INVENTION: LEAST ONE NATURAL OR RECOMBINANT SPIDER SILK OR AN
TITLE OF INVENTION: ANALOG
FILE REFERENCE: 6388-0365-0
CURRENT APPLICATION NUMBER: US/09/247,806
CURRENT FILING DATE: 1999-02-11
EARLIER APPLICATION NUMBER: FR 98/01614
EARLIER FILING DATE: 1998-02-11
LANGE 104 NUMBER: 1998-02-11
LANGE 104 NUMBER: 1998-02-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 14
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INFORMATION FOR SEQ ID NO:
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APPLICATION NUMBER: 08/077,60
EPILING DATE: JUNE 15, 1993
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
NAME: CR-9
                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 651
APPLICANT: Lewis, Randolph V.
APPLICANT: Xu, Ming
APPLICANT: Hinman, Michael B.
TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SI
TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: unknow
TOPOLOGY: unknown
MOLECULE TYPE: protein
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LENGTH: 651 amino acids
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                                                                                                                                                                                                                                                                  293 GAAAAGGA 300
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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Pred. No.
                                                                                                                                                                                                                                                                                                       Mismatches
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   A TRANSFORMED CELL
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RESULT 25
US-08-317-844B-2
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ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1447
TELECOMMUNICATION INFORMATION:
TELEFAX: (703) 205-8000
TELEFAX: (703) 205-8050
                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/317,844B
FILING DATE: 04-OCT-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                     APPLICANT: Xu, Ming
APPLICANT: Hinman, Michael B.
APPLICANT: HINMAN, Michael B.
TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK
TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL
TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF
                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 62

CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: 301 No. 5989894th Washington Street
CITY: Falls Church
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 718 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    317 GAAAAGGA 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      293 GAAAAGGA 300
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                 COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/0
FILING DATE: 19-APR-1995
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STREET: 301 No. 5728810th Washington Street
CITY: Falls Church
STATE: Virginia
COUNTRY: U.S.A.
                                                                                                                                                                                                                    22046
Murphy Jr., Gerald M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Randolph V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.6%; Scc.
/ 100.0%; Pre
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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US-09-034-177-3
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                   Query Match
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Patent No. 6127146
                                                                                                                                                   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 747 amino acids
                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERSKE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
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TELEX: 243345
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 718 milino acids
                                                                                             IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: DOS
SOFTWARE: FBS4TSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/034,177
FILING DATE: HEREWITH
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lal, Preeti
APPLICANT: Guegler, Karl J.
APPLICANT: COLLEY, Neil C.
TITLE OF INVENTION: HUMAN F:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
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REFERENCE/DOCKET NUMBER: 14.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 241-1300
TELEFAX: (703) 241-2848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
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STREET: 3174 Por
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                             LIBRARY: GenBank
CLONE: GI 1174414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
ZIP: 943
                                                                                                               TOPOLOGY:
                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE:
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                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                    TELEFAX:
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les 8; Conserv
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                                                                                                         linear
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100.0%;
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rive 0; Mismatches
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Score 8;
Pred. No.
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Pred. No.
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Best Local Similarity

Length 747;

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RESULT 28
US-09-548-372D-13
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Best Local Similarity
Watches 8; Conserva
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US-08-630-915A-37
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          Sequence 13, Application US/09548372D
Patent No. 6420534
GENERAL INFORMATION:
APPLICANT: GURNEY ET AL.
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE,
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 29915/62801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No.
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CURRENT APPLICATION NUMBER: US/09/548,372D
                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/6
FILING DATE: 03-APR-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MISTOCK, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: FOWLKES, Dank ...

APPLICANT: MCCONNELL, Stephen J.

TITLE OF INVENTION: POLYPEPFIDES HAVING A FUNCTIONAL

TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                       307
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APPLICANT: KAY, Brian K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                         294 AAAAGGAA 301
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                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
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ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                     AAAAGGAA 314
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                                                                                                                                                                                                                                                                                                                                                                                                                         1400 amino acids
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1155 Avenue of the Americas
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                                                                                                                                                                                                                                                                     Conservative
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100.0%; Pred. N
tive 0; Misma
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o. 1.3e+02;
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                                                 APP SUBSTRATES THEREFOR AND USES
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; Sequence 1, Application US/09738884
; Patent No. 6391606
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN P
; TITLE OF INVENTION: NUCLEIC ACID MO
TITLE OF INVENTION: PROTEINS, AND U
                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens US-09-548-367D-13
                                                                                                                                                                                RESULT 30
US-09-738-884-1
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US-09-548-367D-13
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PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881
PRIOR APPLICATION NUMBER: US 60/101,594
PRIOR FILING DATE: 1998-09-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 13
LENGTH: 2088
TYPE: PRT
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SEQ ID NO 13
LENGTH: 2088
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: GURNEY ET AL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Patent No. 6440698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USE TITLE OF INVENTION: THEREOF FILE REFERENCE: 29915/6280H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/548,367D CURRENT FILING DATE: 2000-04-12
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PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 73
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PRIOR FILING DATE: 1999-09-23
PRIOR EPILIOR DATE: 1999-09-23
PRIOR FILING DATE: 1999-09-23
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                     FILE REFERENCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                       297 AGGAAGAA 304
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                                                                                                                                                                                                                                                                                                                                                 Conservative
NUMBER: US/09/738,884
                                      KARI et al
ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
NUCLEIC ACID MOLECULES ENCODING HUMAN
PROTEINS, AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                  1.6%; Score 8; DB 4; Le 100.0%; Pred. No. 1.9e+02;
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100.0%; Pred. No.
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1.9e+02
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                                                           HUMAN PHOSPHOLIPASE
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US-09-436-063C-7
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; TYPE: PRT
; ORGANIZM: Caenorhabditis elegans
US-09-627-650B-7
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Best Local Similarity
"hehes 8; Conserve
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; ORGANISM: Human
US-09-738-884-1
                                                         CURRENT APPLICATION NUMBER: US/99/436,063C CURRENT FILING DATE: 1999-11-08 PRIOR APPLICATION NUMBER: 60/107727 PRIOR FILING DATE: 1998-11-09 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 100.0%;
Best Local Similarity 100.0%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                             Sequence 7, Application US/09436063C Patent No. 6407210
                                                                                                                                                                         APPLICANT: Bamber, Bruce
APPLICANT: Jorgensen, Erik
TITLE OF INVENTION: Nematode Neuromuscular Junction GABA Receptors and
TITLE OF INVENTION: Methods Related Thereto
FILE REFERENCE: P-1095corrected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 7
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TITLE OF INVENTION: Mematode Neuromuscular Junction GABA Receptors and
TITLE OF INVENTION: Methods Related Thereto
FILE REFERENCE: 21101.0009U3
CURRENT APPLICATION NUMBER: U5/09/627,650B
CURRENT FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 09/436,063
PRIOR APPLICATION NUMBER: 09/436,063
PRIOR FILING DATE: 1999-11-08
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                                 LENGTH: 2508
TYPE: PRT
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PRIOR FILING DATE: 1998-11-09
NUMBER OF SEO ID NOS: 50
SOFTWARE: Patentin Ver. 2.1
           ORGANISM: Caenorhabditis elegans
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NUMBER OF SEQ ID NOS: 5

SOFTWARE: FastSEQ for Windows Version 4.0
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No. 2.3e+02;
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US-09-627-650B-3
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                                                                      Matches
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 2544
TYPE: PRT
ORGANISM: Caenorhabditis elegans
                                                                                                                                                                                                                                         APPLICANT: Jorgensen, Erik
TITLE OF INVENTION: Nematode Neuromuscular Junction GABA Receptors and
TITLE OF INVENTION: Methods Related Thereto
FILE REFERENCE: P-1095corrected
CURRENT APPLICATION NUMBER: US/09/436,063C
CURRENT FILING DATE: 1999-11-08
PRIOR APPLICATION NUMBER: 60/107727
PRIOR FILING DATE: 1998-11-09
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Best Local Similarity
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Best Local Similarity 100.
Change 8; Conservative
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SOFTWARE: PatentIn Ver. 2.1
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APPLICANT: Jorgensen, Erik
TITLE OF INVENTION: Nemattode Neuromuscular Junction GABA Receptors and
TITLE OF INVENTION: Methods Related Thereto
FILE REFERENCE: 21101.000903
                                                                                                                                                  TYPE: PRT ORGANISM: Caenorhabditis elegans
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PRIOR APPLICATION NUMBER: 09/436,063
PRIOR FILING DATE: 1999-11-08
PRIOR APPLICATION NUMBER: 60/107,727
PRIOR FILING DATE: 1998-11-09
NUMBER OF SEC 17. WIG 1998-11-09
NUMBER OF SEC 17. WIG 1998-11-09
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CURRENT FILING DATE: 2000-07-28
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1184 GAAGAAAA 1191
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                                299 GAAGAAAA 306
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100.0%; Pred. No. 2.;
tive 0; Mismatches
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Pred. No.
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No. 2.3e+02;
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5. 2.3e+02;
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RESULT 37
US-09-336-447A-76
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                                                                   Sequence 76, Application US/09336447A Patent No. 6310190 GENERAL INFORMATION:
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Matches
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LENGTH: 2601
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TITLE OF INVENTION: Nematode Neuromuscular Junction GABA Receptors and
TITLE OF INVENTION: Methods Related Thereto
FILE REFERENCE: 21101.0009U3
CURRENT APPLICATION NUMBER: US/09/627,650B
CURRENT FILING DATE: 2000-07-28
              APPLICANT: HANSEN, ERIC J.
APPLICANT: AEBI, CHRISTOF
APPLICANT: COPE, LESLIE D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Nematode Neuromuscular Junction GABA Receptors and TITLE OF INVENTION: Methods Related Thereto FILE REFERENCE: P-1095corrected CURRENT APPLICATION NUMBER: US/09/436,063C CURRENT FILING DATE: 1999-11-08
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PRIOR FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 18
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PRIOR FILING DATE: 1999-11-08
PRIOR APPLICATION NUMBER: 60/107,727
PRIOR FILING DATE: 1998-11-09
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AEBI, CHRISTOPH
COPE, LESLIE D.
MACIVER, ISOBEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jorgensen, Erik
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100.0%; Pr
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D. 2.3e+02;
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Query Match
Best Local Similarity
"""+"hes 8; Conserv:
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US-08-425-069-5
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5178861-16
;PATENT NO. 5178861
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; PATENT NO. 5178861
; PATENT NO. 5178861
; NUSSENZWEIG, RUTH S.; NUSSENZWEIG, VICTOR N.
; NUSSENZWEIG, RUTH S.; NUSSENZWEIG, VICTOR N.
; TITLE OF INVENTION: CROSS-REACTIVE AND PROTECTIVE EPITOPES
;OF CIRCUMPROPOROLITE PROTEINS
; NUMBER OF SEQUENCES: 18
; CURRENT APPLICATION DATA:
;CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db
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; LOCATION: (1036)..(3786)
; OTHER INFORMATION: Xaa =
US-09-336-447A-76
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Best Local Similarity
Matches 7; Conserv
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CURRENT APPLICATION NUMBER: US/09/336,447A
CURRENT FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 98
                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Lewis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: FISKE, MICHAEL J. APPLICANT: FREDENBURG, ROSS A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Moraxella catarrhalis FEATURE:
                                                    APPLICANT: Lewis, Randolph V.
APPLICANT: Xu, Ming
APPLICANT: Xu, Ming
APPLICANT: Hinman, Michael B.
TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK
TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL
TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESCEP: 11-22 CT.
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APPLICATION NUMBER: 115,634
FILING DATE: 26-OCT-1987
APPLICATION NUMBER: 649,903
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ADDRESSEE: Birch, Stewart, Kolasch & Birch STREET: 301 No. 5728810th Washington Street CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 11
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FILING DATE: 22-JUN-1989
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Pred. No.
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Pred. No.
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o. 3.4e+02;
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COUNTRY:

U.S.A.

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Sequence 5, Application
Patent No. 5989894
GENERAL INFORMATION:
APPLICANT: Lewis, F
APPLICANT: Xu, Ming
APPLICANT: Hinman,
                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 40
US-08-317-844B-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-425-069-5
COUNING.
COUNING.
ZIP: 22046
ZIP: 22046
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
TOWNSTER: IBM PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: 301 No. 5989894th Washington Street
CITY: Falls Church
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                      APPLICANT: Hinman, Michael B.
TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER STIK
TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL
TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF
NUMBER OF SEQUENCES: 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,069
FILING DATE: 19-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            294 AAAAGGA 300
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3 AAAAGGA 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 1447-106P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald
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OTHER INFORMATION:
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Murphy Jr., Gerald M
REGISTRATION NUMBER: 28,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                              Xu, Ming
                                                                                                                                                                                                                                                                                                                               Lewis, Randolph V.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= alanine_stretch
/note= "this segment of alanines in the repeat
unit can also contain 7 alanine residues."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= repeat_unit
/note= "spider silk protein repeat unit"
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Pred. No.
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5. 17;
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US-07-987-286-3
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Best Local Similarity
"-+-hes 7; Conserv
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                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application 07/987286
PATENT NO. 5500366
GENERAL INFORMATION:
APPLICANT: RUSSELL-JONES, GREGORY J
APPLICANT: GECZY, ANDREW F
TITLE OF INVENTION: T-CELL EPITOPES
NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 21 amino acids
          CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UNMBER: PCT/AU91/00429
FILING DATE: 17-SEP-1991
PRIOR APPLICATION DATA:
                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: 07/987,286
FILING DATE: 16-MAR-1993
                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                 COUNTRY: UCCOUNTRY: UCCOUNTRY: UCCOUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1447-105P
TELECOMMUNICATION INFORMATION:
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MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
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CURRENT APPLICATION DATA
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NAME: Murphy Jr., Gerald
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                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
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TELEFAX: 248345
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                          CITY: WASHINTON, D.C.
                                                                                                                                                                                                                                                                                       ADDRESSEE: FOLEY & LARDNER STREET: 3000 K STREET, N.W.
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OTHER INFORMATION:
OTHER INFORMATION:
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LOCATION:
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 21 amino TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (703) 241-1300
TELEFAX: (703) 241-2848
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FILING DATE: 04-OCT-1994
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100.0%; Pred. No. 17;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= alanine_stretch
/note= "this segment of alanines in the punit can also contain 7 alanine residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= repeat_unit
/note= "spider silk protein repeat unit"
AU PK2361
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                                                                                                                                                   Version #1.25
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US-08-614-626-3
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; TOPOLOGY: 1:
; MOLECULE TYPE:
US-08-614-626-3
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Best Local S
Matches 7
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                                                                                        TELEX: 904136
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K STREET, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 16
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
                                                                                                                                                                                                                                FILING DATE: 17-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PIFILING DATE: 18-SEP-1990
                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/987,286
FILING DATE: 16-MAR-1993
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                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 202 672 5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: T-CELL EPITOPES NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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                                                                                                          TELEPHONE: ZUZ V. S399
                                                                                                                                                                NAME: BENT, STEPHEN A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16
                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/614,626 FILING DATE: CLASSIFICATION:
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10 GAAVGAA 16
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les 7; Conserv
                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/AU91/00429 FILING DATE: 17-SEP-1991
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                                                          LENGTH:
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                                           amino acid
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                                                        23 amino acids
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GECZY, ANDREW F
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                                linear
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                peptide
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100.0%; Pr
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                                                                                                                                                                    16786/175/CHAC
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Pred. No.
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                                                                                                         NAME/KEY: Modified;
LOCATION: 25
OTHER INFORMATION:
US-07-987-286-11
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Best Local Similarity
Matches 7; Conserv
                                                    Matches
                                                                  Query Match
Best Local :
                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 202 672 5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PK2361
FILING DATE: 18-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: T-CELL EPITOPES NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: RUSSELL-JONES, GREGORY JAPPLICANT: GECZY, ANDREW F
                                                                                                                                                                                                                                                                                                                         TELLEFAX: 200
TELEFAX: 904136
                       289 GAAVGAA 295
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11 GAAVGAA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/
FILING DATE: 17-SEP-1991
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                                                                                                                                                                              OTHER INFORMATION:
                                                                                                                                                                                          OTHER INFORMATION:
                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 29,768 REFERENCE/DOCKET NUMBER: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE:
                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                          NAME: BENT, STEPHEN A. REGISTRATION NUMBER: 2
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                                                                                                                                                                                                                      NAME/KEY:
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5. 5500366
                                                 Similarity 100 7; Conservative
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                                                                                                                                                                                                                                                                              amino acid
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3000 K STREET, N.W.
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                                                 100.0%; P
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100.0%;
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ACID"
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                                                 1.4%; Score 7; DB 1; 00.0%; Pred. No. 20; ve 0; Mismatches
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s; Pred. No. 18;
0; Mismatches
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                                                                                                                        "RESIDUE
                                                                                                                                                                                            "RESIDUE 1 IS PYROGLUTAMIC
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18;
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Sequence 24, Appitume Sequent No. 5500366 Patent No. 5500360 GENERAL INFORMATION:

Application 07/987286

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Query Match
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                                                                                                                                                                                                                                       Sequence 38, Application US/08425069 Patent No. 5728810
                                                                               GENERAL INFORMATION:
GENERAL INFORMATION: APPLICANT: Lewis, Randolph V.
APPLICANT: Yu, Ming
APPLICANT: Hinman, Michael B.
APPLICANT: Hinman, Michael B.
TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK
TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL
TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:

APPLICATION NUMBER: AU PK2361
FILING DATE: 18-SEP-1990
ATTORNEY/AGENT INFORMATION:

NAME: BENT, STEPHEN A.

REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 1678:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: 301 No. 5728810th Washington Street
CITY: Falls Church
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LENGTH: 25 amino acids
TYPE: amino acid
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APPLICATION NUMBER: PCT/AU91/00429
FILING DATE: 17-SEP-1991
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: GECZY, ANDREW F
TITLE OF INVENTION: T-CELL EPITOPES
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEB: FOLEY & LARDNER
ADDRESSEB: FOLEY & LARDNER
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                  289 GAAVGAA 295
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TELEFAX: 904136
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QУ
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; LOCATION: 1..25
; OTHER INFORMATION:
US-08-425-069-38
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Search completed: January 27, 2003, 16:37:39 Job time: 41 secs
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Best Local :
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                                                                                                                                                                                                                                                                                                                 TOPOLOGY: not relevant
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
TRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Murphy Jr., Gerald M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
STRANDEDNESS: not relev
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APPLICATION NUMBER: US/0
FILING DATE: 19-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION: NAME: Murphy Jr., Gerald
                                                                                                                                                                                                                                                                                                               FRAGMENT TYPE:
                                                                                            294 AAAAGGA 300
                                                                                                                                             Local Similarity
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ZIP: 220
                                                                                                                                                                                                                                                                              ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 19
CLASSIFICATION:
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22046
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100.0%; Pred. No.
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Best Local Similarity
Matches 9; Conser
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                                                  ABB58615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             preventing cell proliferative disorders (e.g. arteriosclerosis, cirrhosis, psoriasis, cancers); endocrine disorders (e.g., type I or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 99-100; 136pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human oxidoreductase protein (ORP) useful for diagnosing, treating and preventing cell proliferative, neurological, viral, reproductive and autoimmune/inflammatory disorders associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yue H,
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  26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    with aberrant ORP expression, in assays to monitor patients being treated with ORP or modulators thereof, and for assessing toxicity of potential
                                                                                                ABB58615 standard; Protein; 696
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(first entry)
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100.0%; Pred. No. 25;
Live 0; Mismatches
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Search completed: January 27, Job time : 60 secs

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Matches 9
                                                                                                                                                    The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABLIG511), expressed DNA sequences (ABLIG175) and the encoded proteins (ABB57037-ABB72072).

(ABB57737-ABB72077), but was obtained in electronic format directly from WIPO specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic a genes from Drosophila interactions -
                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 2637;
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N-PSDB; ABL02718.
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11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster polypeptide SEQ ID NO 2637
                                                                                                         Sequence
                                                                                                                                       at ftp.wipo.int/pub/published_pct_sequences.
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                                                                          Length 696;
                                             Indels
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                                             Gaps
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RESULT 43
AAB12164
ID AAB12
XX AAB12
XX AAB12
XX AAB12
XX Pydrc
XX Hydrc
XX Humar
KW Fooll
KW Homar
KW biopil
KW haem
KW auto:
XX Homo
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  17-NOV-1998;
22-DEC-1998;
16-MAR-1999;
27-APR-1999;
19-MAY-1999;
                                                                                                                                                                                                                                                                                                                      proliferation control; differentiation induction; material transport; biophylaxis; signal receptor; ion channel; transporter; immunostimulant; immunosuppressant; haematopoiesis regulator; chemotactic; chemokinetic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition; autoimmune disease; Alzheimer's disease; Parkinson's disease; cancer.
                                                                                                                                            17-NOV-1999;
                                                                                                                                                                                           25-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, haematopoiesis regulating activity intibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                       WO200029448-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hydrophobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB12164 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tang
Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note: Records for SEQ ID NO 2110 (AAK52581), (AAM80020) are omitted as the relevant pages were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding polypeptides with cytokine-like activities useful in diagnosis and gene therapy \boldsymbol{\cdot}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            280 GAGLAGLAA 288
|||||||||
37 GAGLAGLAA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-476283/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-OCT-2000;
30-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HYSE-) HYSEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                         sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  secreted protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Liu C,
Wang D,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page 280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         domain protein from clone HP10673 isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
98JP-0326255.
98JP-0364315.
99JP-0069811.
99JP-0119299.
99JP-0138169.
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2000US-0728422.
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                                                                                                                                          99WO-JP06412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drmanac RT, Asundi V
Wang J, Zhang J, Ro
Wejhrman T, Goodrich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.8%; 5-
100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                             membrane protein; hydrophobic domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 9; DB 2
Pred. No. 24;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Asundi V, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB
24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22;
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F, (
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from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 518;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the sequence listing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (AAK52582) and 3666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R, C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from Thymus cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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RESULT 44
AAB73670
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                      arteriosclerosis; cirrhosis; psoriasis; cancer; endocrine disorder; diabetes mellitus; diabetes insipidus; dwarfism; hirsutism; amenorrhoea; osteoporosis; metabolic disorder; obesity; phenylketonuria; hypercholesterolaemia; reproductive disorder; infertility; ovulatory defect; menstrual cycle defect; endometriosis; polycystic ovary disease; spermatogenesis disruption; impotence; neurological disorder; epilepsy; stroke; Alzheimer's disease; Huntington's disease; Parkinson's disease; Creutzfeldt-dakob disease; meningitis; cerebral palsy; muscular dystrophy; mood disorder; anxiety; schizophrenic disorder; infection; autoimmune disorder; entermatery.
                                                                                                                      inflammatory disorder; acquired immunodeficiency syndrome; AIDS; asthma; allergy; Crohn's disease; atopic dermatitis; gout; multiple sclerosis; rheumatoid arthritis; ulcerative colitis; drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     channels and transporters. The present sequence is a human protein which has at least one hydrophobic domain. This protein may be a secretory or a membrane protein. The present protein may have cytokine and cell proliferation/differentiation activity, immune stimulating or suppressing activity, haematopoiesis activity, tissue growth activity, haemostatic and thrombolytic activity, anti-inflammatory activity and tumour treatment of activity, anti-inflammatory activity and tumour treatment of autolimune disease, Alzheimer's disease, Parkinson's
                                                                              Homo sapiens
                                                                                                               toxicity
                                                                                                                                                                                                                                                                                                                                                                                                                11-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB73670 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Secretory proteins play important roles in the proliferation control, differentiation induction, the material transport and the biophylaxis cells. Membrane proteins have important roles as signal receptors, ior
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Secretory proteins play implifiementiation induction,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 376-378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            activities e.g. immunomodulatory, antiinflammatory, chemokinetic, hemostatic, thrombolytic -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proteins comprising hydrophobic regions, such as secretory and membrane proteins, useful in research and diagnostics and having various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAA62067, AAA62077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              280 GAGLAGLAA 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PROT-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SAGA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAGLAGLAA 39
                                                                                                                                                                                                                                                                                                                                      oxidoreductase protein; ORP; cell proliferative disorder;
                                                                                                                                                                                                                                                                                                                                                                            oxidoreductase protein ORP-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                s,
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9; Conser
                                                                                                             screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SAGAMI CHEM RES PROTEGENE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 555 AA;
                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cancer.
                                                                                                           transgenic animal; SNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         410pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 9;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB
. 25;
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                                                                                                                                                                                                                                                                                                          amenorrhoea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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of
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/label= 41..555

signal\_peptide

Location/Qualifiers

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RESULT 41
AAM78562
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                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
03-FEB-2000;
27-APR-2000;
20-JUN-2000;
19-JUL-2000;
01-SEP-2000;
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28-NOV-1997;
17-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY36754-Y37949 are encoded by open reading frames (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). The polypeptides can be used as vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye diseases such as conventional trachoma, nonendemic trachoma, and inclusion conjunctivitis; genital diseases such as nongonococcal uretritis, epidymitis, cervicitis, salpingitis, perihepatitis, bartholinitis; pneumopathy in breast feeding infants; and venereal lymphogranulomatosis. The polypeptides of the invention may be of use in treating these diseases.
                                                                                                                                                                    Human; cytokine; cell proliferation; cell differentiation; gene th vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 1271-1272; 1755pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-371125/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Griffais R;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chlamydia trachomatis
                                                                    05-FEB-2001;
                                                                                          09-AUG-2001
                                                                                                              WO200157190-A2
                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                  Human
                                                                                                                                                                                                                                       06-NOV-2001
                                                                                                                                                                                                                                                                                   AAM78562 standard; Protein; 513 AA.
                                                                                                                                                                                                                                                                                                                                          446
                                                                                                                                                                                                                                                                                                                                                                447
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                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
les 9; Conser
                                                                                                                                                                                                                                                                                                                                          FWQQASKIA 454
                                                                                                                                                                                                                                                                                                                                                              FWQQASKIA 455
                                                                                                                                                                                                                  protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence of Chlamydia trachomatis
                                                                                                                                                          system
                                                                                                                                                                                                                                                                                                                                                                                                                                   481
 2000US-0560875.
2000US-0598075.
2000US-0620325.
2000US-0654936.
                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                             2000US-0496914.
                                                                    2001WO-US04098
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97FR-0015041.
97FR-0016034.
                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
                                                                                                                                                         disorder; arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98WO-IB01939
                                                                                                                                                                                                                  IJ
                                                                                                                                                                                                                                                                                                                                                                                                1.8%;
                                                                                                                                                                                                                  NO 1224.
                                                                                                                                                                                                                                                                                                                                                                                      0,
                                                                                                                                                                                                                                                                                                                                                                                                Score 9; |
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                            inflammation
                                                                                                                                                                                                                                                                                                                                                                                         DB
22;
                                                                                                                                                                                                                                                                                                                                                                                                           20;
                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                          Length 481;
                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                          therapy;
                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                      RESULT 42
AAM79546
  Q
                                                                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                Matches
        03-FEB-2000;
27-APR-2000;
20-JUN-2000;
19-JUL-2000;
01-SEP-2000;
                                                                                                                                                                   Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-476283/51.
N-PSDB; AAK51695.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xue
                                                                             05-FEB-2001;
                                                                                                                                                                                                                           Human protein SEQ ID
                                                                                                                                                                                                                                                06-NOV-2001
                                                                                                                                                                                                                                                                                             AAM79546 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
  15-SEP-2000
                                                                                                   09-AUG-2001.
                                                                                                                        WO200157190-A2
                                                                                                                                               Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                         280 GAGLAGLAA 288
                                                                                                                                                                                                                                                                                                                                                    31 GAGLAGLAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YTY,
                                                                                                                                                                                                                                                                                                                                                                                                Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYSEQ INC.
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Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                             513 AA;
2000US-0560875.
2000US-0598075.
2000US-0620325.
2000US-0654936.
2000US-0663561.
                                                                                                                                                                                                                                                (first entry)
                                                       2000US-0496914.
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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM73323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, inmunomodulatory activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-SEP-2000; 2000US-0663561
20-OCT-2000; 2000US-0693325
30-NOV-2000; 2000US-0728422
                                                                                                                                                                                                                                                                                                     Claim 20; Page 3481-3482; 6221pp; English.
                                                                                              Note: Records for SEQ ID NO 2110 (AAK52581), (AAM80020) are omitted as the relevant pages
                                                                                                                                                                                                                                                                                                                                  useful in diagnosis and gene therapy
                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding polypeptides with cytokine-like activities
                                                                                   were missing at the time of publication.
Conservative
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Wang J,
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J, Zhang J, Ren
an T, Goodrich R
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    DB . 23;
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F, C
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120-AUG-1999
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27-AUG-1999
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27-AUG-1999
31-AUG-1999
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GAGLAGLAA 64
                        GAGLAGLAA 288
                                                   Similarity
9; Conserv
                                                Conservative
                                                                                                99US-0158232

99US-0158294

99US-0159294

99US-0159293

99US-0159330

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99US-0159637

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99US-0160767

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99US-0149923

99US-0149930

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99US-0149175.
99US-0149426.
                                                           100.0%;
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                                             Score 9; DB 2; Pred. No. 18; 0; Mismatches
                                                0;
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                                                                     Length 382;
                                             Indels
                                            0;
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RESULT. 39
ABB9226

ID ABB92

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AC ABB92

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AC ABB92

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DT 31-M
DE Herb
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                   Vaccine; eye disease; conventional trachoma; nonendemic trachoma; paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis; nongonococcal uretritis; epidymitis; cervicitis; salpingitis;
              bartholinitis;
                                                                                      Protein which is
                                                                                                                      07-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as herbicides.
                                                                                                                                                    AAY37632;
                                                                                                                                                                                 AAY37632 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequence from plant with nucleic acid or amino acid sequences from non-plant organisms -
                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 5; SEQ ID NO 1467; 261pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-269010/31.
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                                                                                                                                                                                                                                                                                       280 GAGLAGLAA 288
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                                                                                                                                                                                                                                                                                                                     Local Similarity
mes 9; Conserv
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                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                            61
            pneumopathy;
                                                                                   specific to Chlamydia trachomatis.
                                                                                                                                                                                 Protein;
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                                                                                                                                                                                 481
       venereal lymphogranulomatosis
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Best Local Similarity 100.0%;
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05-MAR 1999
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23-MAR 1999
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06-APR 1999
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23-APR 1999
24-MAY 1999
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06-MAY 1999
11-MAY 1999
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53 GAGLAGLAA 61
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99US-012845
99US-0130047
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06-11 06-12 06-13 06-13			70T-1 70T-1	70L-1	701-1 701-1	101-1 101-1	7011	7011 7011	JUL-1 JUL-1	JUN-1	JUN-1	JUN-	NDC	JUN-	JUN-	JUN	JUN	JUN-	NDL-	JUN-	JUN-	-NDC-
27-JUL-1999; 28-JUL-1999; 02-AUG-1999; 02-AUG-1999; 02-AUG-1999; 03-AUG-1999; 04-AUG-1999;	9999	999;	999;	999;	999;	999;	999;	999;	999;	; 6661 (6661 (6661	, 6661 (6661 (1999)	,6661	1999;	1999;	1999;	1999;	1999; 1999;	1999;	1999;	1999;	1999; 1999;	1999;
990S-0145919. 990S-0145951. 990S-0146386. 990S-0146388. 990S-0146389. 990S-0147038. 990S-0147204.	S-014 S-014 S-014	S-014 S-014	IS-014	7S-01	78-01 78-01 78-01	JS-01	JS-01 JS-01 JS-01	JS-01 JS-01	US-01 US-01 US-01	US-01 US-01 US-01	US-01 US-01 US-01	US-01	US-01	US-01	us-01	US-01	US-01	US-01	US-01	0S-01	US-01	0-SD(
5919. 5951. 6386. 6388. 6389. 7038. 7204.	5218 5224 5276 5913 5918	5085 5087 5192	14884 14814 15086 15088	14334	14331 14332 14333	14085	43542 43624 44005	42803 42920 42977	42154 42055 42390	40991 41287 41842	40354 40695 40823	39899	39750 39763	39462	39459	39457	3945	3949	3945	3884	13809	L3752
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26-OCT-1999; 990 26-OCT-1999; 990 26-OCT-1999; 990 26-OCT-1999; 990 28-OCT-1999; 990 28-OCT-1999; 990 28-OCT-1999; 990	22-OCT-1999; 990 22-OCT-1999; 990 22-OCT-1999; 990 25-OCT-1999; 990 25-OCT-1999; 990	21-OCT-1999; 99t 21-OCT-1999; 99t 21-OCT-1999; 99t 21-OCT-1999; 99t 21-OCT-1999; 99t	14-0CT-1999; 990 14-0CT-1999; 990 18-0CT-1999; 990 21-0CT-1999; 990	13-OCT-1999; 990 14-OCT-1999; 990 14-OCT-1999; 990 14-OCT-1999; 990	12-OCT-1999; 991 13-OCT-1999; 991 13-OCT-1999; 991	06-OCT-1999; 991 07-OCT-1999; 991 08-OCT-1999; 991	29-SEP-1999; 991 04-OCT-1999; 991 05-OCT-1999; 991	23-SEP-1999; 991 24-SEP-1999; 991 28-SEP-1999; 991	10-SEP-1999; 99 20-SEP-1999; 99 22-SEP-1999; 99	10-SEP-1999; 99 13-SEP-1999; 99 15-SEP-1999; 99	01-SEP-1999; 99 07-SEP-1999; 99	R 27-AUG-1999; 99 R 30-AUG-1999; 99	20-AUG-1999; 99 27-AUG-1999; 99 27-AUG-1999: 99	23-AUG-1999; 99 25-AUG-1999; 99	20-AUG-1999; 99 20-AUG-1999; 99 23-AUG-1999: 99	18-AUG-1999; 99 20-AUG-1999; 99	16-AUG-1999; 99	13-AUG-1999; 99	11-AUG-1999; 99	09-AUG-1999; 99	06-AUG-1999; 99 09-AUG-1999; 99	05-AUG-1999; 99
PR 28-0CT-1999; 99US-016 PR 26-0CT-1999; 99US-016 PR 26-0CT-1999; 99US-016 PR 28-0CT-1999; 99US-016 PR 28-0CT-1999; 99US-016 PR 28-0CT-1999; 99US-016 PR 28-0CT-1999; 99US-016	22-OCT-1999; 990 22-OCT-1999; 990 22-OCT-1999; 990 25-OCT-1999; 990 25-OCT-1999; 990	21-OCT-1999; 99t 21-OCT-1999; 99t 21-OCT-1999; 99t 21-OCT-1999; 99t 21-OCT-1999; 99t	14-0CT-1999; 990 14-0CT-1999; 990 18-0CT-1999; 990 21-0CT-1999; 990	13-OCT-1999; 990 14-OCT-1999; 990 14-OCT-1999; 990 14-OCT-1999; 990	12-OCT-1999; 991 13-OCT-1999; 991 13-OCT-1999; 991	06-OCT-1999; 991 07-OCT-1999; 991 08-OCT-1999; 991	29-SEP-1999; 991 04-OCT-1999; 991 05-OCT-1999; 991	23-SEP-1999; 991 24-SEP-1999; 991 28-SEP-1999; 991	10-SEP-1999; 99 20-SEP-1999; 99 22-SEP-1999; 99	10-SEP-1999; 99 13-SEP-1999; 99 15-SEP-1999; 99	01-SEP-1999; 99 07-SEP-1999; 99	R 27-AUG-1999; 99 R 30-AUG-1999; 99	20-AUG-1999; 99 27-AUG-1999; 99 27-AUG-1999: 99	23-AUG-1999; 99 25-AUG-1999; 99	20-AUG-1999; 99 20-AUG-1999; 99 23-AUG-1999: 99	18-AUG-1999; 99 20-AUG-1999; 99	16-AUG-1999; 99	13-AUG-1999; 99	11-AUG-1999; 99	09-AUG-1999; 99	06-AUG-1999; 99 09-AUG-1999; 99	05-AUG-1999; 99
26-OCT-1999; 990 26-OCT-1999; 990 26-OCT-1999; 990 26-OCT-1999; 990 28-OCT-1999; 990 28-OCT-1999; 990 28-OCT-1999; 990	22-OCT-1999; 990 22-OCT-1999; 990 22-OCT-1999; 990 25-OCT-1999; 990 25-OCT-1999; 990	21-OCT-1999; 99t 21-OCT-1999; 99t 21-OCT-1999; 99t 21-OCT-1999; 99t 21-OCT-1999; 99t	14-0CT-1999; 990 14-0CT-1999; 990 18-0CT-1999; 990 21-0CT-1999; 990	13-OCT-1999; 990 14-OCT-1999; 990 14-OCT-1999; 990 14-OCT-1999; 990	12-OCT-1999; 991 13-OCT-1999; 991 13-OCT-1999; 991	06-OCT-1999; 991 07-OCT-1999; 991 08-OCT-1999; 991	29-SEP-1999; 991 04-OCT-1999; 991 05-OCT-1999; 991	23-SEP-1999; 991 24-SEP-1999; 991 28-SEP-1999; 991	10-SEP-1999; 99 20-SEP-1999; 99 22-SEP-1999; 99	10-SEP-1999; 99 13-SEP-1999; 99 15-SEP-1999; 99	01-SEP-1999; 99 07-SEP-1999; 99	R 27-AUG-1999; 99 R 30-AUG-1999; 99	20-AUG-1999; 99 27-AUG-1999; 99 27-AUG-1999: 99	23-AUG-1999; 99 25-AUG-1999; 99	20-AUG-1999; 99 20-AUG-1999; 99 23-AUG-1999: 99	18-AUG-1999; 99 20-AUG-1999; 99	16-AUG-1999; 99	13-AUG-1999; 99	11-AUG-1999; 99	09-AUG-1999; 99	06-AUG-1999; 99 09-AUG-1999; 99	05-AUG-1999; 99
26-OCT-1999; 26-OCT-1999; 26-OCT-1999; 28-OCT-1999; 28-OCT-1999; 28-OCT-1999;	22-OCT-1999; 990 22-OCT-1999; 990 22-OCT-1999; 990 25-OCT-1999; 990 25-OCT-1999; 990	21-OCT-1999; 99t 21-OCT-1999; 99t 21-OCT-1999; 99t 21-OCT-1999; 99t 21-OCT-1999; 99t	14-0CT-1999; 990 14-0CT-1999; 990 18-0CT-1999; 990 21-0CT-1999; 990	13-OCT-1999; 990 14-OCT-1999; 990 14-OCT-1999; 990 14-OCT-1999; 990	12-OCT-1999; 991 13-OCT-1999; 991 13-OCT-1999; 991	06-OCT-1999; 991 07-OCT-1999; 991 08-OCT-1999; 991	29-SEP-1999; 991 04-OCT-1999; 991 05-OCT-1999; 991	23-SEP-1999; 991 24-SEP-1999; 991 28-SEP-1999; 991	10-SEP-1999; 99 20-SEP-1999; 99 22-SEP-1999; 99	10-SEP-1999; 99 13-SEP-1999; 99 15-SEP-1999; 99	01-SEP-1999; 99 07-SEP-1999; 99	R 27-AUG-1999; 99 R 30-AUG-1999; 99	20-AUG-1999; 99 27-AUG-1999; 99 27-AUG-1999: 99	23-AUG-1999; 99 25-AUG-1999; 99	20-AUG-1999; 99 20-AUG-1999; 99 23-AUG-1999: 99	18-AUG-1999; 99 20-AUG-1999; 99	16-AUG-1999; 99	13-AUG-1999; 99	11-AUG-1999; 99	09-AUG-1999; 99	06-AUG-1999; 99 09-AUG-1999; 99	05-AUG-1999; 99
26-OCT-1999; 990 26-OCT-1999; 990 26-OCT-1999; 990 26-OCT-1999; 990 28-OCT-1999; 990 28-OCT-1999; 990	22-OCT-1999; 990 22-OCT-1999; 990 22-OCT-1999; 990 25-OCT-1999; 990 25-OCT-1999; 990	21-OCT-1999; 99t 21-OCT-1999; 99t 21-OCT-1999; 99t 21-OCT-1999; 99t 21-OCT-1999; 99t	14-0CT-1999; 990 14-0CT-1999; 990 18-0CT-1999; 990 21-0CT-1999; 990	13-OCT-1999; 990 14-OCT-1999; 990 14-OCT-1999; 990 14-OCT-1999; 990	12-OCT-1999; 991 13-OCT-1999; 991 13-OCT-1999; 991	06-OCT-1999; 991 07-OCT-1999; 991 08-OCT-1999; 991	29-SEP-1999; 991 04-OCT-1999; 991 05-OCT-1999; 991	23-SEP-1999; 991 24-SEP-1999; 991 28-SEP-1999; 991	10-SEP-1999; 99 20-SEP-1999; 99 22-SEP-1999; 99	10-SEP-1999; 99 13-SEP-1999; 99 15-SEP-1999; 99	01-SEP-1999; 99 07-SEP-1999; 99	R 27-AUG-1999; 99 R 30-AUG-1999; 99	20-AUG-1999; 99 27-AUG-1999; 99 27-AUG-1999: 99	23-AUG-1999; 99 25-AUG-1999; 99	20-AUG-1999; 99 20-AUG-1999; 99 23-AUG-1999: 99	18-AUG-1999; 99 20-AUG-1999; 99	16-AUG-1999; 99	13-AUG-1999; 99	11-AUG-1999; 99	09-AUG-1999; 99	06-AUG-1999; 99 09-AUG-1999; 99	05-AUG-1999; 99

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical inaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human
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                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
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                                                                                                                                                                                                                                                                                                                                   Claim 20; SEQ ID No 36219; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drmanac RT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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les 9; Conser
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9;
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RESULT 37
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Best Local Similarity
Matches 9; Conser
      14 - MAY 1999;
14 - MAY 1999;
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18 - MAY 1999;
19 - MAY 1999;
20 - MAY 1999;
21 - MAY 1999;
24 - MAY 1999;
25 - MAY 1999;
27 - MAY 1999;
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30-APR-1999;
03-APR-1999;
05-MAY-1999;
06-MAY-1999;
06-MAY-1999;
07-MAY-1999;
11-MAY-1999;
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21-APR-1999;
23-APR-1999;
23-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the specification, but was obtained in electronic format directly
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06-APR-1999
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23-MAR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana protein fragment SEQ ID NO:
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                                                                                                                                                                                                                            99US-0128714.
99US-0129845.
99US-0130077.
                        99US-0132485.
99US-0132487.
99US-0132863.
99US-0134219.
99US-0134219.
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99US-0134219.
99US-0134270.
99US-0134768.
99US-0134941.
99US-0135124.
99US-013553.
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99US-0132407.
99US-0132484.
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99US-0130510.
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5. 17;
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AAY93594-Y93605 are encoded by differentially expressed human goassociated with disease states and disorders. The specification describes methods preventing, diagnosing and treating cardiac, land inflammatory diseases associated with inappropriate express.
                                                                                                                  Preventing, diagnosing and treating cardiac, kidney and inflammatory disorders using cardiac genes that are differentially expressed in disease states such as cardiac arrhythmia and arteriosclerosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Differentially expressed human gene; cardiac disease; kidney disease; inflammatory disease; I-8U; prostacyclin-stimulating factor; isf-2; tissue specific mRNA; insulin-like growth factor binding protein 6; OSF-1; gas-1; YME; BYC2; pre-B cell stimulating factor homologue; SDF peripheral benzodiazepine receptor; annexin II cellular ligand; pl1; congenital heart failure; dilated congestive cardiomyopathy;
                                                                                      Disclosure;
                                                                                                                                                                                        N-PSDB;
                                                                                                                                                                                                           WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     kidney failure) and to delay or prevent the development of PKD-associated hypertension, bleeding into the cysts, pain, and renal insufficiency associated with the progression of cystic disease. In an exemplification of the invention, the expression profile of representative genes was examined in a rat model of polycystic kidney disease and compared with gene expression in normal rats. The PTBR gene (also referred to as clone PO242) was found to be overexpressed by a factor of 2 in the rat model of PKD, while the DBI gene was underexpressed by a factor of 1.9. The present sequence represents the amino acid sequence of human PTBR.
Note: The present sequence is not given in the specification although it is referred to as SEQ ID NO:3 and is stated as being given in figure 2.
This sequence was obtained using the DNA sequence given in figure 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypertrophic cardiomyopathy; restrictive cardiomyopathy; mitral valve disease; aortic valve disease; tricuspid valve disease, angina pectoris; myocardial infarction; cardiac arrhythmia;
                                                                                                                                                                                                                                                                                                           18-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo
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DB; AAA46678.
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9; Conserv
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                                                                                                                                                                                                                                                                          SCIOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                         White
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                           98US-0113008
                                                                                                                                                                                                                                                                                                                                          99WO-US29941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
                                                                                      8K;
                                                                                                                                                                                                                                          孲,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.8%; J.
100.0%; Pr
... 0;
                                                                                      170pp; English
                                                                                                                                                                                                                                         Damm
                                                                                                                                                                                                                                       DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 9; |
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                       Lewicki JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 21;
. 8.9;
                                                                                                                                                                                                                                     Joly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 169;
                                                                                                                                                                                                                                     A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptor
                   cardiac, kidney
                                                                                                                                                                                                                                     Schreiner GF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                  genes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SDF1a;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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expression

Sequences AAB37984-B38019 represent the amino acid sequences of 27 human secreted proteins encoded by the genes AAC69084-C69119. The genes and proteins are useful for preventing, ameliorating or treating medical conditions, e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic diagnosis, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer, and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital.

disease,

Disclosure;

Page 27; 453pp;

English.

New nucleic acid molecules encoding 27 human secondingnosing, preventing, treating or ameliorating

secreted proteins ting medical condit

conditions

and

for

food additives or preservatives

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Вþ
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AAB38041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        differentially expressed cardiac, kidney and inflammatory genes (e.g. AAA4668-79). These genes include I-8U, prostacyclin stimulating factor, isf-2, tissue specific mRNA, insulin-like growth factor binding protein 6, OSF-1, gas-1, YMP, BTG2, pre-B cell stimulating factor homologue (SDF1a), peripheral benzodiazepine receptor, and cellular ligand of annexin II (pl1), respectively. These diseases include congenital heart failure, dilated congestive cardiomyopathy, ypertrophic cardiomyopathy, restrictive cardiomyopathy, mitral valve disease, aortic valve disease, tricuspid valve disease, angina pectoris, arterial hypertension, renovascular hypertension, arteriosclerosis,
                                                                                                                                                                                                  WPI; 2000-594448/56
                                                                                                                                                                                                                                                                                                       16-MAR-2000; 2000WO-US06783
                                                                                                                                                                                                                                                                                                                                                                                                        Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antinifiammatory; antidicer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparastic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
                                                                                                                                                                                                                         Komatsoulis
                                                                                                                                                                                                                                                                                                                               21-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                            Homo
                                                                                                                                                                                                                                                                                                                                                                                                  neurological disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB38041 standard; Peptide; 172
                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                  18-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                     WO200055371-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fragment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB38041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     atherosclerosis and/or cardiac tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 GAAAATTVA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        302 GAAAATTVA 310
                                                                                                                                                                                                                                                                                                                                                                           sapiens
                                                                                                                                                                                                                                    MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
9; Conserv
                                                                                                                                                                                                                                  N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             169 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                  J,
                                                                                                                                                                                                                                                                                 99US-0125055
                                                                                                                                                                                                                       Lafleur
                                                                                                                                                                                                                                    Ebner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.8%;
                                                                                                                                                                                                                                                                                                                                                                                                  infection; human;
                                                                                                                                                                                                                    DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein encoded by gene 10 clone HWHGP71.
                                                                                                                                                                                                                                 Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 9; I
                                                                                                                                                                                                                      Moore PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                     Shi Y,
Olsen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB
8.
                                                                                                                                                                                                                                                                                                                                                                                               secreted protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21;
,.9;
                                                                                                                                                                                                                     Birse C,
HS, Young
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                               Florence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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RESULT 32
AAY42438
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-OCT-1999
22-OCT-1999
25-OCT-1999
25-OCT-1999
26-OCT-1999
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26-OCT-1999
26-OCT-1999
28-OCT-1999
28-OCT-1999
29-OCT-1999
                                                                                                                    This is the amino acid sequence of the peripheral-type benzodiazepine receptor, derived from the human breast cancer cell lines, MCF-7 and MDA-231. The amino acid sequence differs from the wildtype PBR sequence with the replacement of histidine 162 with arginine and replacement of alanine 147 with a threonine.

This invention provides the means of Peripheral-type benzodiazepine
                                                                                                                                                                                                                                                                                                                      Agents
useful
                                   receptor (PBR) modulation.

Molecules that inhibit PBR function are used to treat diseases mediated by increased cell proliferation, particularly cancers (e.g. mediated by increased cell proliferation, particularly cancers, live cancers of the lung, stomach, prostate, overy, testes, pancreas, live cancers of the lung, stomach, prostate, overy, testes, pancreas, live cancers of the lung, stomach, prostate, overy, testes, pancreas, live cancers of the lung, stomach, prostate, overy, testes, pancreas, live cancers of the lung, stomach, prostate, overy, testes, pancreas, live cancers of the lung, stomach, prostate, overy, testes, pancreas, live cancers of the lung, stomach, prostate, overy, testes, pancreas, live cancers of the lung, stomach, prostate, overy, testes, pancreas, live cancers of the lung, stomach, prostate, overy, testes, pancreas, live cancers of the lung, stomach, prostate, overy, testes, pancreas, live cancers of the lung, stomach, prostate, overy, testes, pancreas, live cancers of the lung, stomach, prostate, overy, testes, pancreas, live cancers of the lung, stomach, prostate, overy, testes, pancreas, live cancers of the lung, stomach, prostate, overy, testes, pancreas, live cancers of the lung, stomach, prostate, overy, testes, pancreas, live cancers of the lung, stomach, prostate, overy, testes, pancreas, live cancers of the lung, stomach, prostate, overy, testes, pancreas, live cancers of the lung, stomach, prostate, overy, testes, pancreas, live cancers of the lung, stomach, prostate, overy, testes, pancreas, live cancers of the lung, stomach, prostate, overy, testes, pancreas, live cancers of the lung, stomach, prostate, overy, live cancers of the lung, stomach, prostate, live cancers of the lung, stomach, live cancers of the lung, stomach, live cancers of the live cancers of the lung, stomach, live cancers of the lung, stomach, live cancers of the lung, stom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer; cell proliferation; invasive tumor; aggressive tumor;
antiproliferative; hypoproliferative; detection; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY42438 standard;
                                                                                                                                                                                                                                                                            Claim 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9949316-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Кeу
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino acid sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Papadopoulos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GEOU ) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       129 GAAAAGGAA 137
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                                                                                                                                                                                                                                                                                                                                                                                                   1999-580494/49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAAAAGGAA
                                                                                                                                                                                                                                                                                                                  that reduce peripheral-type benzodiazepine receptor function, for detecting and treating aggressive phenotype breast cancer
                      vagina, skin, esophagus, nasopharyns,
                                                                                                                                                                                                                                                                                                                                                                                    AAZ22636, AAZ22637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
9; Conserv
                                                                                                                                                                                                                                                                            Page 74-75; 76pp; English.
  peripheral nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GEORGETOWN MEDICAL CENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first
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99US-0160989.
99US-0161404.
99US-0161405.
99US-0161360.
99US-0161361.
99US-0161361.
99US-0161361.
99US-0161920.
99US-0161922.
99US-0161993.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US06515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Culty M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein; 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of partial PBR from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               e 9;
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MDA-231 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21;
  and
                      oropharynx,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnosis
cartilage), especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MCF-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytostatic;
                                                                                                                                                                                                                                                                                                                      cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                         liver,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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RESULT 33
AAB11966
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      Qy
The invention relates to a method for the treatment and prevention of CC diseases that involve cyst formation, particularly polycystic kidney Cd diseases (PKD), comprising administering a ligand of a peripheral-type CC disease (PKD), comprising administering a ligand can also be used for the CC treatment of hypertension associated with PKD. The invention also cencompasses the diagnosis and/or prognosis of cystic disease, or the CC diagnosis of a predisposition to cystic disease, via the monitoring of CC changes in expression levels of PTBR or an endogenous ligand of PTBR, CC such as the diazepam binding inhibitor (DBI). In PKD, the PTBR gene is CC overexpressed, while the natural ligand is underexpressed. The PTBR CC ilgands of the invention inhibit the proliferation of epithelial cells. CC from PKD kidneys, i.e., they arrest cell growth but do not kill cells. CC The method is used to treat diseases associated with cyst formation, particularly both the autosomal dominant and recessive forms of PKD. The methods can also be used for the diagnosis and prognosis of a cystic disease or susceptibility to it. The methods may also be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     breast cancer. PBR, or a vector encoding PBR may diseases mediated by reduced cell proliferation, % \left( 1\right) =\left( 1\right) ^{2}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polycystic kidney disease; PKD; hy insufficiency; autosomal dominant cystic disease; PTBR ligand; diffe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                            Treatment and prevention of cystic disea kidney disease, by administering ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-DEC-1998;
26-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peripheral-type benzodiazepine receptor; polycystic kidney disease; PKD; hyperten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human peripheral-type benzodiazepine receptor (PTBR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB11966 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            retardation.
                                                                                                                                                                                                                                                                               Example 1;
                                                                                                                                                                                                                                                                                                                                                                          N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                       Schreiner GF, Joly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200037085-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypotensive
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SCIO-) SCIOS INC.
(STAN/) STANTON L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 GAAAATTVA 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAAAATTVA 310
                                                                                                                                                                                                                                                                                                                                                                                        2000-442524/38
                                                                                                                                                                                                                                                                                                                                                                          AAA72048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                               Page -;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             169
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99US-0136208.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTBR ligand; differential expression; antiproliferative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Σ
                                                                                                                                                                                                                                                                            37pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein; 169
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                                                                                                                                                                                                                                                                                                                                                                                                                        White
                                                                                                                                                                                                                                                                                English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                        꼽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                receptor; PTBR; human; cyst formation; hypertension; renal failure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    torm;
                                                                                                                                                                                                                                                                                                                            disease, specifically polycystic igand of peripheral benzodiazepine
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8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   autosomal recessive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          such as developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        be used to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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פי סי	ָּאַק אָק אָק אָק אָק אָק אָק
21-MAY 1999 22-MAY 1999 25-MAY 1999 27-MAY 1999 27-MAY 1999 27-MAY 1999 01-JUN 1999 01-JUN 1999 01-JUN 1999 01-JUN 1999 10-JUN 1999 11-JUN	1-MAY-1999; 4-MAY-1999; 4-MAY-1999; 4-MAY-1999; 4-MAY-1999; 8-MAY-1999; 9-MAY-1999; 9-MAY-1999;
990S-0135353 990S-0135629 990S-0136329 990S-0136392 990S-0137528 990S-0137528 990S-0137529 990S-0139540 990S-0139452 990S-0139453 990S-0139453 990S-0139454 990S-0139456 990S-0139460 990S-0139460 990S-0139461 990S-0139461 990S-0139463 990S-0139463 990S-014963 990S-014053 990S-014053 990S-014065 990S-014065 990S-014083 990S-014083 990S-0144884 990S-0144884 990S-0144884 990S-0144884 990S-0144884 990S-0144884 990S-0144884 990S-0144884 990S-0144886	99US-0134256. 99US-0134218. 99US-0134219. 99US-0134221. 99US-0134370. 99US-0134768. 99US-0134941. 99US-0135124.
יט קר	ק ק ק ק ק ק ק ק ק ק ק ק ק ק ק ק ק ק ק
20-A 20-A 20-A 20-A 20-A 20-A 20-A 20-A	23-JUL 23-JUL 26-JUL 27-JUL 27-JUL 27-JUL 28-JUL 02-AUG
22-AUG 23-AUG 30-AUG 30-AUG 30-AUG 30-AUG 30-AUG 30-AUG 30-AUG 30-AUG 31	23-JUL-1999; 99US-0145; 23-JUL-1999; 99US-0145; 26-JUL-1999; 99US-0145; 27-JUL-1999; 99US-0145; 27-JUL-1999; 99US-0145; 27-JUL-1999; 99US-0145; 28-JUL-1999; 99US-0145; 28-JUL-1999; 99US-0145;

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56 GAAAAGGAA

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RESULT 30
ABG41659
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26-MAY-2000;
30-JUN-2000;
          (a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single gene, comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several tissues and/or cell types using hybridisation to a single exon microarrays having a probe with the exon, where a common pattern of expression of the exons in the tissues and/or cell types indicates that
                                                                                                                                                                                                     The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes; the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung; measuring gene expression in a sample derived from human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung mRNA, and (b) measuring the label detectably bound to each probe of the array; identifying exons in a enkaryotic genome, comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chronic obstructive pulmonary disease; interstitial lung dis familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG41659 standard; Peptide; 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human peptide encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spatially-addressable set of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MOLE-) MOLECULAR DYNAMICS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hanzel DK,
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2000US-234687P.
2000US-236359P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-180312P.
2000US-207456P.
2000US-0608408.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ID No 31324; 634pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen W,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human lung samples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rank DR
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assigned to a single gene; a peptide

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 RESULT 31
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25-FEB-1999
05-MAR-1999
09-MAR-1999
23-WAR-1999
25-WAR-1999
01-APR-1999
01-APR-1999
116-APR-1999
116-APR-1999
21-APR-1999
21-APR-1999
23-APR-1999
23-APR-1999
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23-APR-1999
23-APR-1999
24-APR-1999
25-APR-1999
26-APR-1999
06-MAY-1999
06-MAY-1999
06-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesis, pulmonary hypertension and hyaline membrane disease. The present sequence is a peptide/protein encoded by a single exon probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probes/open reading frames (ORF). The probes are used for gene probes/open reading frames (ORF). The probes are used for gene particularly using human lung derived mRNA and for the study of lung diseases such as asthma, lung cancer, chronic obstructive pulmonary disease (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                          Protein identification; hybridisation assay; ger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana protein fragment SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG11693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAG11693 standard; Protein; 159
                                                                                                                                                                                                                                                                                                       25-FEB-2000;
                                                                                                                                                                                                                                                                                                                                  06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       haemosiderosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of 12011 sequences,
                                                                                                                                                                                                                                                                                                                                                                                                               termination sequence
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9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       153
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                                                                                                                                                                                                                                                                                                       2000EP-0301439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                          99US-0129845.
99US-0130077.
99US-0130510.
99US-0130510.
99US-0130891.
99US-0131449.
99US-0132048.
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-S066
-S066
-S066
                                       -S066
-S066
-S066
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99US-0128714.
                                                                                                                                                                                                99US-0127462
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                                                                                                                                                                                                                                     99US-0123548
99US-0125788
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                                      -0132484.
-0132485.
                                                                  -0132407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mentioned in the specification, or encoded frames (ORF). The probes are used for gene
                                                                                                                                                                                                                                                                                                                                                                                                                           genetic mapping; gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                         signal transduction pathway; metabolic pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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RESULT 28
AAM19335
ID AAM19
XX AAM19
AX AAM19
AX 12-OC
DE Pepti
XX Probe
KW Cervi
XX Homo
XX Homo
XX HOMO
OP-AI
XX 30-JF
PR 26-MF
PR 27-SI
PR 27-SI
PR 27-SI
PR 27-SI
PR 21-SI
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Best Local
The present invention relates to human single exon nucleic acid probes (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical
                                                                                                                                                                                                                                                                                                                                                                                                                                       04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
30-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                                                     (MOLE-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cervical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Probe; human; microarray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide #5769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAM19335 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention
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                                                                                                                                                                                                                                                                          2001-488901/53.
                                                                                                                                                                                                                                                                                                                         SG,
                                                                                                                                                          27;
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                                                                                                                                                                                            genome-derived single exon nucleic acid probes useful for zing gene expression in human cervical epithelial cells
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                                                                                                                                                                                                                                                                                                                                                                  MOLECULAR DYNAMICS
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9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer.
                                                                                                                                             SEQ ID No 24161; 487pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                              ; 2000US-0207456.
; 2000US-0608408.
; 2000US-0632366.
; 2000US-0233687.
; 2000US-0233689.
; 2000US-0236359.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein; 153
                                                                                                                                                                                                                                                                                                                      Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             by probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   provides a number of single exon nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene
                                                                                                                                                                                                                                                                                                                      Σ
                                                                                                                                                                                                                                                                                                                                                                     INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 9; DB 2
Pred. No. 8.1
0; Mismatches
                                                                                                                                                                                                                                                                                                                    Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for measuring cervical gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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ΩV

293 GAAAAGGAA

Query Match Best Local S Matches 9

Similarity 9; Conser

1.8%; llarity 100.0%; Conservative (

0;

Mismatches

0

Indels

0;

Gaps

0;

Score 9; Pred. No.

DB 22; 5. 8.1;

Length 153

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RESULT 29
AAM32131
ID AAM32
XX
AC AAM32
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
         such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived human placenta. The probes are useful for antenatal diagnoci----
                                                                                                                                                                                      21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                 04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
Sequence
                                                                                   Claim 27;
                                                                                                     analyzing
                                                                                                                                                   Penn
                                                                                                                                                                                                                                                                                  09-AUG-2001
                                                                                                                                                                                                                                                                                                     WO200157272-A2
                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                 Probe; microarray;
                                                                                                                                                                                                                                                                                                                                                                   Peptide #6168 encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Note: The sequence data for this patent did not specification, but was obtained in electronic for at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                     (MOLE-)
                                                                                                                                                                                                                                                                30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                         genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                     17-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                         AAM32131;
                                                                                                                                                                                                                                                                                                                                                                                                                           AAM32131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cervical cancer.
Note: The sequen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   epithelial cells. By measuring gene useful in grading and/or staging of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          293 GAAAAGGAA 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56 GAAAAGGAA 64
                                                                                                                                2001-488897/53.
                                                                                                                                                   SG,
                                                                                                  genome-derived single exon nucleic acid zing gene expression in human placenta -
                                                                                                                                                                    MOLECULAR DYNAMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
9; Conser
                                                                              SEQ ID No 32400; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
                                                                                                                                                  Hanzel DK,
153
                                                                                                                                                                                     2000US-0180312.
2000US-0207456.
2000US-068408.
2000US-0632366.
2000US-0234687.
2000US-0234687.
2000US-02346359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  153 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                               2001WO-US00663
                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
AA;
                                                                                                                                                                                                                                                                                                                                                 human;
                                                                                                                                                                                                                                                                                                                                                                                                                          Protein; 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.
                                                                                                                                                 Chen W,
                                                                                                                                                                                                                                                                                                                                                                   by probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .0%;
                                                                                                                                                                                                                                                                                                                                                placenta;
                                                                                                                                                                   INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
Pred.
                                                                                                                                                  Rank DR;
                                                                                                                                                                                                                                                                                                                                                                for measuring placental gene
                                                                                                                                                                                                                                                                                                                                                                                                                          A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . 9
. 9
                                                                                                                                                                                                                                                                                                                                               antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expression, diseases of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . BB
                                                                                                            probes useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probes are therefore cervix, notably
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         part of the printed directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                 expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     notably
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                                                   by one
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RESULT 26
AAM59299
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                                                                                                                                                                                                                                                                          Matches
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                          The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart (see ABA21355-ABA41305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; gene expression; heart; microarray; vascular system; cardiovascular disease; hypertension; cardiac arrhythmia; congenital heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-AUG-2001
                                                       Human; brain expressed exon; gene expression analysis; microarray; Alzheimer's disease; multiple sclerosis; so
                                                                                           Human brain expressed single exon probe encoded protein SEQ ID
                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JAN-2001; 2001WO-US00666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200157274-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
WO200157275-A2
                     Homo sapiens
                                            epilepsy;
                                                                                                                    05-NOV-2001
                                                                                                                                                                  AAM59299 standard; Protein; 153 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MOLE-)
                                                                                                                                                                                                                                        293 GAAAAGGAA 301
                                                                                                                                                                                                                              56
                                                                                                                                                                                                                                                                          Local Similarity
les 9; Conserv
                                                                                                                                                                                                                                                                                                                                                  ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                              GAAAAGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULAR DYNAMICS INC
                                             cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 25516;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hanzel
                                                                                                                                                                                                                                                                                                                           153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0180312.

2000US-0207456.

2000US-0608408.

2000US-0632366.

2000US-0234687.

2000US-0236359.
                                                                                                                                                                                                                                                                           Conservative
                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000GB-0024263.
                                                                                                                                                                                                                              64
                                                                                                                                                                                                                                                                                                                           ₽,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DK,
                                                                                                                                                                                                                                                                                       1.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         530pp; English
                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                       Score 9;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rank DR;
                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for analyzing gene expression
                                                                                                                                                                                                                                                                                       DB 22;
. 8.1;
                                                        sclerosis; schizophrenia
                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                  Length 153;
                                                                                                                                                                                                                                                                           Indels
                                                                     probe;
                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'n
                                                                                             NO:
                                                                                                                                                                                                                                                                          Gaps
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RESULT 27
AAM71846
ID AAM71
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                Matches
                            04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                         probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                    Human; bone marrow expressed exon;
microarray; cancer; leukaemia; lymp
                                                                                                                                                                                                                                                                                   AAM71846 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-483446/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-AUG-2001
                                                                                                     30-JAN-2001; 2001WO-US00668
                                                                                                                         09-AUG-2001.
                                                                                                                                              WO200157276-A2
                                                                                                                                                                                                                    Human
                                                                                                                                                                                                                                          06-NOV-2001
                                                                                                                                                                                                                                                               ААМ71846;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention provides a number of single exon nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JAN-2001;
(MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MOLE-)
                                                                                                                                                                                                                                                                                                                                                           293 GAAAAGGAA 301
                                                                                                                                                                                                                                                                                                                                       56 GAAAAGGAA 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SG,
                                                                                                                                                                                                                     bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                Similarity
9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO:
                                                                                                                                                                                                                   marrow expressed
                                                                                                                                                                                                                                                                                                                                                                                                                       153
                  2000US-0180312.
2000US-0207456.
2000US-0508408.
2000US-0632366.
2000US-0234687.
2000US-0236539.
2000US-0236539.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0207456.
2000US-0608408.
2000US-0632368.
2000US-0234687.
2000US-0234687.
2000US-0236359.
2000CB-0024263.
                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0180312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001WO-US00667
                                                                                                                                                                                                                                                                                                                                                                                                                        Ą,
                                                                                                                                                                                                                                                                                    Protein;
                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probes
                                                                                                                                                                                                                                                                                    153
                                                                                                                                                                                                                    probe encoded protein SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                               Score 9; DB 2; Pred. No. 8.1
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              650pp + Sequence Listing; English
                                                                                                                                                                                    con; gene expression analysis; probe;
lymphoma; myeloma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rank DR;
                                                                                                                                                                                                                                                                                    A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                         22;
.1;
                                                                                                                                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                                                                                                                                                                  Length 153
                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                0;
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אר א א א מר א מר א מר א א מר א מ
 QΥ
                                               Query Match
Best Local S
                                    Matches
                                                                                                    14-OCT-1999

14-OCT-1999

14-OCT-1999

14-OCT-1999

11-OCT-1999

21-OCT-1999

21-OCT-1999

21-OCT-1999

21-OCT-1999

21-OCT-1999

22-OCT-1999

22-OCT-1999

22-OCT-1999

25-OCT-1999

25-OCT-1999

26-OCT-1999

26-OCT-1999

28-OCT-1999

28-OCT-1999

28-OCT-1999

28-OCT-1999

29-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-SEP-1999
20-SEP-1999
22-SEP-1999
23-SEP-1999
24-SEP-1999
24-SEP-1999
28-SEP-1999
29-SEP-1999
04-OCT-1999
06-OCT-1999
07-OCT-1999
07-OCT-1999
13-OCT-1999
13-OCT-1999
13-OCT-1999
13-OCT-1999
13-OCT-1999
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20-AUG-1999
23-AUG-1999
23-AUG-1999
25-AUG-1999
25-AUG-1999
27-AUG-1999
27-AUG-1999
27-AUG-1999
30-AUG-1999
31-AUG-1999
31-AUG-1999
01-SEP-1999
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13-SEP-1999;
15-SEP-1999;
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10-AUG-1999;
11-AUG-1999;
11-AUG-1999;
12-AUG-1999;
293 GAAAAGGAA 301
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20-AUG-1999,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-AUG-1999;
17-AUG-1999;
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                                  Similarity
9; Conser
                                  Conservative
                                                                                                    99US-0161406
99US-0161359
99US-0161360
99US-0161361
99US-0161920
99US-0161992
99US-0161993
99US-0162142
                                                                                                                                                                                                                                                                                                               99US-0158369

99US-0159293

99US-0159294

99US-0159295

99US-0159329

99US-0159330

99US-0159331

99US-0159637

99US-0159637

99US-0169767

99US-01607761

99US-01607768

99US-0160770

99US-0160770

99US-0160814

99US-0160815
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99US-0160989.
99US-0161404.
99US-0161405.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0157865.
99US-0158029.
99US-0158232.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0149722.
99US-0149929.
99US-0149929.
99US-0150566.
99US-015066.
99US-0151065.
99US-0151066.
99US-01511080.
99US-0151303.
99US-0151403.
99US-0151403.
99US-0151403.
99US-015139.
99US-015139.
99US-0153758.
99US-0154018.
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99US-0157117.
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99US-0149175.
99US-0149426.
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99US-0148171.
99US-0148319.
99US-0148341.
99US-0148565.
                         1.8%; >c.
100.0%; Pr
                                               Score 9;
; Pred. No
                               mismatches
                                             DB 21;
5. 7.9;
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                                                              Length 149;
                             Indels
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RESULT 25
ABB23746
ID ABB23
XX
AC ABB23
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DT 23-JA
XX
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Best Local Similarity
Whiches 9; Conserv?
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ABB38670
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Protein #5745 encoded by probe for measuring heart cell gene expression.
                                                                                                                                                                                                                                              The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                             23-JAN-2002
                                                     ABB23746;
                                                                          ABB23746 standard;
                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                  Claim 27; SEQ ID NO 31305; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
                                                                                                                                                                                                                                                                                                                                                                                           Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Penn SG,
                                                                                                                                                 293 GAAAAGGAA 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; foetal liver; gene expression; single exon nucleic acid probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hanzel DK,
                                                                                                                                                                                                                               153 AA;
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                           (first entry)
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
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                                                                          Protein; 153
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RESULT 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana protein
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88 GAAAAGGAA 96
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RESULT 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AABO8324-36 represent epitopes derived from a Chlamydia pneumoniae protein. The protein, immunogenic fragments of it, nucleotide sequences encoding it, or inhibitor specific against it are used to manufacturing a medicament for the treatment of infection due to C. pneumoniae. An antibody specific against the protein can diagnose a C. pneumoniae infection. C. pneumoniae infection can be prevented. Artherosclerosis, including coronary atherosclerosis, caused by C. pneumoniae can also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 5; Page 34; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New Chlamydia pneumoniae protein of 496 amino acids for diagnosing, preventing and treating C. pneumoniae infection and atherosclerosis
                                                           Allergens derived from Cladosporium herbarum spores - also recombinant DNA for expressing the allergens, useful for in vitro allergy detection
Spores of Cladosporium herbarum are the most common fungal spores found in the air; they can cause allergic reactions. Various Clah
                                   Claim 1; Page 25; 35pp; German.
                                                                                                           WPI; 1995-106850/14.
N-PSDB; AAQ87846.
                                                                                                                                                                                                                                                                                                                                             Fungal spore; allergen; Clahll; allergy; ribosomal protein; RLA2
                                                                                                                                                                                                                                                                                                                                                                     Cladosporium herbarum allergen Clahll.
                                                                                                                                                                                                                                                                                                                                                                                                25-OCT-1995
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                                                                                                                                                                      Achatz G,
                                                                                                                                                                                                                       27-AUG-1993;
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Unger A;
                                                                                                                                                                         Breitenbach M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein; 111
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                                                                                                                                                           Oberkofler H,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 9;
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AAG11695
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09 - MAR-1999
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30 - APR-1999
30 - APR-1999
31 - MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      allergens and sequences encoding them have now been isolated. The mature Clahil allergen has mol. wt. 11 kD and is encoded by cDNA sequence AAQ87846. The allergen has homology to the ribosomal protein RLA2. Potential epitopic subfragments were identified by computer analysis of the amino acid sequence. See AAR72670-R72674 for potential B-cell epitopes and AAR72675-R72677 for potential T-cell epitopes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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9; Conser
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9905-0128714
9905-0120875
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RESULT 19
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AAB08333 standard; Peptide;
                                                                                                                                                                 AAB08324-36 represent epitopes derived from a Chlamydia pneumoniae protein. The protein, immunogenic fragments of it, nucleotide sequences encoding it, or inhibitor specific against it are used to manufacturing a medicament for the treatment of infection due to C. pneumoniae. An antibody specific against the protein can diagnose a C. pneumoniae infection. C. pneumoniae infection can be prevented. Artherosclerosis, including coronary atherosclerosis, caused by C. pneumoniae can also
                                                                                                                                                                                                                                                                             New Chlamydia pneumoniae protein of 496 amino acids for diagnosing, preventing and treating \mathcal C. pneumoniae infection and atherosclerosis, including coronary atherosclerosis -
                                                                                                                                          Sequence
                                                                                                                                                                                                                                                          Claim 5; Page 34; 35pp; English.
                                                                                                                                                                                                                                                                                                                                               Burnie JP,
                                                                                                                                                                                                                                                                                                                                                                   (NEUT-) NEUTEC PHARMA PLC
                                                                                                                                                                                                                                                                                                                                                                                        05-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             coronary atherosclerosis; epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Epitope derived from a hlamydia pneumoniae protein.
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                                                                                                                                                              prevented
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nes 9; Conser
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9; Conserv
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Pred. No.
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7.8e+05;
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RESULT 20
AAB08334
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Matches
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                                                                  Chlamydia pneumoniae
                                                                                        coronary
                                                                                                  Chlamydia pneumoniae protein;
                                                                                                                                             04-DEC-2000
                                                                                                                                                                                    AAB08334 standard; Peptide; 9
                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 5; Page 34; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         New Chlamydia pneumoniae protein of 496 amino acids preventing and treating C. pneumoniae infection and including coronary atherosclerosis -
                                                                                                                                                                 ААВ08334;
                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                             127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      coronary atherosclerosis; epitope.
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9; Conserv
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                                                                                        atherosclerosis;
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                                                                                                                                          (first entry)
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                                                                                                                    a hlamydia pneumoniae protein.
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Pred. No.
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7.8e+05;
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28-JAN-2000; 2000WO-GB00237

10-AUG-2000.

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02-JUN-2000;
07-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA).

Note: The sequence data for this patent did not form part of the printed as pecification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful treating acne vulgaris -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polypeptides. The proteins and their associated DNA sequences ar
the treatment, prevention and diagnosis of medical conditions ca
P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L'maisonneuve J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Skeiky YAW,
05-FEB-1999;
                                                                                                                 Chlamydia pneumoniae
                                                                                                                                             coronary atherosclerosis;
                                                                                                                                                            Chlamydia pneumoniae protein;
                                                                                                                                                                                         Epitope derived
                                                                                                                                                                                                                        04-DEC-2000
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                           28-JAN-2000; 2000WO-GB00237
                                                                                                                                                                                                                                                                                AAB08324 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                  10;
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                                                                                                                                                                                                                                                                                Peptide;
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                                                                                                                                                            infection; artherosclerosis;
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                       AAB08324-36 represent epitopes derived from a Chlamydia pneumoniae protein. The protein, immunogenic fragments of it, nucleotide sequences encoding it, or inhibitor specific against it are used to manufacturing a medicament for the treatment of infection due to C. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    An antibody specific against the protein can diagnose a C. pneumoniae infection. C. pneumoniae infection can be prevented. Artherosclerosis, including coronary atherosclerosis, caused by C. pneumoniae can also be prevented or treated
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An antibody specific
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SAKLETPEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000-543485/49
                                                                                                                                                                    5; Page 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   coronary atherosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                    Matthews
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matthews
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99GB-0002555
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                                                                                                                                                                    35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide; 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein; infection; artherosclerosis;
against the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pneumoniae infection and atherosclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 9;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 21; L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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RESULT 14
AAO14994
ID AAO14
XX AAO14
XX AAO14
XX O6-AL
XX Lamir
XX Lamir
XX Lamir
XX Lamir
XX Carci
KW Carci
KW epith
                                                                                                                                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                                                                                                                                                                      QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Creceptor/ligand, antihinflammatory activity, tumour inhibition activity, can and antihinfective activity, and may also be involved in the determination of bodily characteristics, fertility and behaviour. OREX proteins, concluded and antibodies may be used in the treatment of cancers, concluded activity disorders such as psoriasis and benign tumours, conterproliferative disorders such as psoriasis and benign tumours, concluded a disorders such as partial and benign tumours, concluded a disorders such as epilepsy and Alzhelmer's disease, concluded a disorders of tissue growth and regeneration, concluded a disorders of tissue growth and regeneration, concluded a disorders of tissue growth and regeneration, concluded a diseases such as diabetes mellitus, hypothyroidism, and cholesterol ester storage disease, and infectious diseases caused by viral, bacterial, concluded a dispersion of the pathogens. ORFX nucleic acids may also be used as a concrete of primers and probes, in the detection of ORFX genomic sequences cor transcripts, in the identification and cloning of homologous concluded acids may additionally be used to produce transgenic animals concluded a dispersion of the produce transgenic animals concluded as a concluded animal of the dispersion of the ore activity of ORFX concluded animals and concluded animals are useful in the dismunogens to generate specific antibodies, which are useful in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                   laminin gamma-2; cancer; laminin gamma-2 chain inhibition; carcinogen inhibition; anti-gamma-2 chain antibody; epithelial cell adhesion; laminin-5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptides at least 80% identical to the ORFI-ORF4534 (Collectively referred to as ORFX) proteins, polynucleotides at least 85% identical to the ORFX nucleic acid sequences, vectors and host cells comprising ORFX polynucleotides, the recombinant production of ORFX proteins, antibodies specific for ORFX proteins, methods of detecting ORFX polynucleotides and polypeptides, methods of screening for modulators of ORFX expression or activity, and methods of screening individuals for a predisposition to an ORFX-associated disorder. The ORFX proteins of the invention have a wide range of bological activities, such as cytokine, cell proliferation, cell differentiation, immune modulation, haematopolesis regulation, thsue growth, angiogenesis, activin, haematopolesis regulation, haematopolesis regulation.
                                                                                                                                                                06-AUG-2002
                                                                                                                Laminin-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chemokinetic activity, haemostatic activity, thrombolytic activity, receptor/ligand, antiinflammatory activity, tumour inhibition activity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and disorders related to organ
                                                                                                                                                                                                              AAO14994;
                                                                                                                                                                                                                                                       AAO14994 standard; Protein; 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequences ABP31028-ABP35561 represent 4534 novel human proteins designated ORF (open reading frame) 1-4534, and sequences ABN75054-ABN79587 represent CDNAs encoding them. The invention also encompasses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 10; Page 491; 2508pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leach MD,
                                                                                                                                                                                                                                                                                                                                                                                                                      281 AGLAGLAAGA 290
                                                                                                                                                                                                                                                                                                                                                                          77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                          AGLAGLAAGA 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l Similarity
10; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABN75498.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          treatment and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shimkets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                              (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA;
                                                                                                                protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          J.08;
O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       monitoring of ORFX-associated diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 10;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0 B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ъв 23;
.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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AAU50055
PF PD XXX
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                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-JAN-2000;
04-OCT-1994;
18-FEB-1997;
                                                                                                                   SAPHO syndrome; synovitis; acne; pustulosis; uveitis; endophthalmitis; bone; joint; centra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    interactions of invasive carcinogens with surrounding tissues - by usi anti-gamma-2 chain antibodies to inhibit the gamma-2 chain biological activity of the invasive carcinogens. The invention also comprises a method for promoting adhesion of epithelial cells by exposing the cell to intact laminin-5 molecules. The first method of the invention is useful for preventing gamma 2 chain interactions of invasive carcinoge with surrounding tissues. The second method of the invention is useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TRYG/)
(KALL/)
                                                                     Propionibacterium acnes
                                                                                              dermatological;
                                                                                                          inflammatory
                                                                                                                                                          Propionibacterium acnes immunogenic protein #10951.
                                                                                                                                                                                    27-FEB-2002
                                                                                                                                                                                                            AAU50055
                                                                                                                                                                                                                                    AAU50055 standard;
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                 for promoting adhesion of cultured epithelial cells. NOTE: The present sequence is shown as a protein in the however in a figure of the invention this sequence is sh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention comprises a method of inhibiting the laminin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                        sequence (see AAL42916).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vitro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modulating laminin 5 for treating cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-434824/46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tryggvason K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-JAN-2001;
                                                                                                                                                                                                                                                                                                  602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PYKE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US2002052307-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unidentified
                                                                                                                                                                                                                                                                                                                         293 GAAAAGGAAG 302
                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                  GAAAAGGAAG
                                                                                                                                                                                                                                                                                                                                                  10;
                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KALLUNKI P. PYKE C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRYGGVASON
                                                                                                                                                                                                                                                                                                                                                                                                  720 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page 34-36; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                    (first entry)
                                                                                                       phthalmitis; bone; joint; central nervous system; ELISA; lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0663147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-175005P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001US-0756071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kallunki P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94US-0317450.
97US-0800593.
                                                                                              osteopathic;
                                                                                                                                                                                                                                    Protein;
                                                                                                                                                                                                                                                                                                                                                            2.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gamma 2 chain interactions of invasive carcinogens and promoting attachment of cultured cells in
                                                                                                                                                                                                                                     755
                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pyke
                                                                                                                                                                                                                                                                                                                                                           Score 10;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ç,
                                                                                                                                                                                                                                                                                                                                                           DB 2
. 4.1;
                                                                                                                                                                                                                                                                                                                                                                      23;
                                                                                                                                 hypertosis; osteomyelitis;
                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                      Length 720
                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  he sequence listing shown to be a DNA
                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   carcinogens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the cells
                                                                                                                                                                                                                                                                                                                                              Gaps
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01-NOV-2001

WO200181581-A2

20-APR-2001; 2001WO-US12865

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RESULT 12
ABB58985
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                                                                                                                                                                                                                                                                                                                                                 Best
                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                   AABO8324-36 represent epitopes derived from a Chlamydia pneumoniae protein. The protein, immunogenic fragments of it, nucleotide sequences encoding it, or inhibitor specific against it are used to manufacturing a medicament for the treatment of infection due to C. pneumoniae. An antibody specific against the protein can diagnose a C. pneumoniae infection. C. pneumoniae infection can be prevented. Artherosclerosis, including coronary atherosclerosis, caused by C. pneumoniae can also
                      23-MAR-2001;
                                               27-SEP-2001
                                                                                           Drosophila melanogaster
                                                                                                                   pharmaceutical.
                                                                                                                             Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                    Drosophila melanogaster polypeptide SEQ
                                                                                                                                                                             26-MAR-2002
                                                                                                                                                                                                                           ABB58985 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                          be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New Chlamydia pneumoniae protein of 496 amino acids preventing and treating C. pneumoniae infection and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Burnie JP, Matthews
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (NEUT-) NEUTEC PHARMA PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-JAN-2000; 2000WO-GB00237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200046359-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chlamydia pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chlamydia pneumoniae protein; infection; artherosclerosis; coronary atherosclerosis; epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Epitope derived from a hlamydia pneumoniae protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04 -DEC - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB08336;
23-MAR-2000; 2000US-191637P
                                                                      WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-AUG-2000
                                                                                                                                                                                                                                                                                                            167 ETPELPKPGVTPRS 180
                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                     1 ETPELPKPGVTPRS
                                                                                                                                                                                                                                                                                                                                                                                                         prevented or treated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000-543485/49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Page 35;
                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        coronary atherosclerosis -
                                                                                                                                                                                                                                                                                                                                                                                   14 AA;
                                                                                                                                                                                                                                                                                                                                     Conservative
                       2001WO-US09231
                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99GB-0002555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35pp; English
                                                                                                                                                                                                                                                                                     14
                                                                                                                                                                                                                                                                                                                                                2.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pneumoniae infection and atherosclerosis,
                                                                                                                                                                                                                            1937
                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                Score 14; pred. No.
                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                DB 21; 1
                                                                                                                                                    ID NO 3747
                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                          Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for diagnosing,
                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                   0;
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(CURA-) CURAGEN CORP

24-MAY-2000; 2000US-206690P 24-MAY-2001; 2001WO-US17076. WO200190366-A2

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RESULT 13
ABP31472
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Best Local S
Matches 11
                                                                                                                                                                                                                                                                  Human; ORF; open reading frame; ORFX; drug screening; diagnosis; disease monitoring; cytokine; cell proliferation; cell differentiation; immune modulation; haematopolesis regulation; tissue growth; angiogenesis; activin; inhibin; chemotactic; chemokinetic; haemostatic; thrombolytic; tumour inhibition; bodily characteristic; fertility; behaviour; cancer; proliferative disorder; neurological disorder; cardiovascular disease; immune system disorder; organ transplantation; tissue growth disorder; tissue regeneration disorder; diabetes mellitus; behaviour; cancer; tissue regeneration disorder; diabetes mellitus; behaviour; disorder; tissue growth disorder; tissue regeneration disorder; diabetes mellitus; behaviour cancer disorder; tissue regeneration disorder; disorder mellitus; behaviour cancer disorder; diabetes mellitus; behaviour cancer disorder; diabetes mellitus; behaviour cancer disorder; disorder mellitus; behaviour cancer disorder disorder disorder; disorder disorde
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLJ6176-ABLJ6511), expressed DNA sequences (ABLO1840-ABLJ6175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions - \,
                                                                                                                                                                                                                hypothyroidism; cholesterol ester storage disease; infection; vasotropic; antipsoriatic; antidiabetic; cytostatic; nootropi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence data for this patent did not form specification, but was obtained in electronic fat ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                  vasotropic; antipsoriatic; antidiabetic; cytostatic; nootropic; neuroprotective; antiatherosclerotic; anticoagulant; thrombolytic; cardiant; hypotensive; antithyroid; antinflammatory; immunomodula dermatological; analgesic; virucide; antibacterial; fungicide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human ORF445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABP31472 standard; Protein; 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 3747; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-JUL-2000; 2000US-0614150.
                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PEKE ) PE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                294 AAAAGGAAGAA 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAAAGGAAGAA 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001-656860/75.
DB; ABL03088.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO:890.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ŀ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 11;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Myers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                  immunomodulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0,
                                                                                                                                                                                                                                                   vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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В
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                                                         Дb
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                                                                                                                                                                  Query Match
Best Local S
Matches 259
                                                                                                                                                                                    The present sequence is the dihydrofolate reductase (DHFR)/
C. pneumoniae polypeptide antigen variant fusion protein.
C. pneumoniae strain YK41 was cultured and genomic DNA extracted
to prep. a lambda gt11 DNA library. The library was then screened
with an anti-YK41 monoclonal antibody (MAb), which was prepd. by
fusing spleen cells from a mouse infected with YK41 with myeloma
p3/NS1/1-Ag4 1 to produce a MAb expressing hydridoma. The DNA
cobtd. was then fused with DHFR DNA and the expression vector
pADA431 to give pCPN53T. The plasmid was used to transform an
E. coli host, which was cultured to give an antigenic polypeptide
fusion protein. The fusion protein and primers and probes derived
contist DNA can be used in assays for the detection of the
antigenic polypeptide antibodies and DNA, respectively, useful in
the diagnosis of C. pneumoniae infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-APR-1995;
20-SEP-1994;
28-APR-1995;
28-APR-1995;
28-APR-1995;
28-APR-1995;
                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant Chlamydia pneumoniae antigen and antibodies to it used for detection and assay of C. pneumoniae e.g. in clinical
                                                                                                                                                                                                                                                                                                                                                                                                                      diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          infection; tusion pro-
variant; Chlamydia pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polypeptide antigen; strain YK41; plasmid; probe; pCPN53T; primer; assay; detection; antibody; diagnosis; infection; fusion protein; dihydrofolate reductase; DHFR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Izutsu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HITB ) HITACHI CHEM CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-SEP-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DHFR/C. pneumoniae antigen variant fusion
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     222
                                                         162
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                             64
                                                                                   4
ASGKDKTSSTTKTETAPQQGVAAGKESSESQKAGADTGVSGAAATTASNTATKIAMQTSI
               ASGKDKTSSTTKTETAPQQGYAAGKESSESQKAGADTGYSGAAATTASNTATKIAMQTSI 123
                                                                   MSISSSSGPDNQKNIMSQVLTSTPQGVPQQDKLSGNETKQIQQTRQGKNTEMESDATIAG
                                                   MSISSSSGPDNQKNIMSQVLTSTPQGVPQQDKLSGNETKQIQQTRQGKNTEMESDATIAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1996-188399/19
DB; AAT14619.
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                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                        Pages 103-107; 128pp; Japanese.
                                                                                                                                                                432
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                                                                                                           Conservative
                                                                                                                                                                ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94JP-0224711.
95JP-0106006.
95JP-0106008.
95JP-0106009.
95JP-0106010.
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/label= dihydrofolate reductase
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                                                                                                                        52.2%;
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                                                                                                           0;
                                                                                                                     Score 259; DB 17;
Pred. No. 3.7e-222;
                                                                                                          Mismatches
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                                                                                                           0
                                                                                                                                   Length
                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  clinical
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                                                                                                       Gaps
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                                                           Query Match
Best Local
                                               Matches
                                                                                             Sequence
                                                                                                                           AABO8324-36 represent epitopes derived from a Chlamydia pneumoniae protein. The protein, immunogenic fragments of it, nucleotide sequences encoding it, or inhibitor specific against it are used to manufacturing a medicament for the treatment of infection due to C. pneumoniae. An antibody specific against the protein can diagnose a C. pneumoniae infection. C. pneumoniae infection can be prevented. Artherosclerosis, including coronary atherosclerosis, caused by C. pneumoniae can also
                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                              New Chlamydia pneumoniae protein of 496 amino acids preventing and treating C. pneumoniae infection and including coronary atherosclerosis -
                                                                                                                                                                                                                                                                                                                                              (NEUT-) NEUTEC PHARMA PLC.
                                                                                                                                                                                                                                                                                                                                                                       05-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                             28-JAN-2000; 2000WO-GB00237
                                                                                                                                                                                                                                                                                                                                                                                                                      10-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200046359-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         coronary atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chlamydia pneumoniae protein; infection; artherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Epitope derived from a hlamydia pneumoniae protein.
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                      223 EKQAIKIDKEREEY 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124
                                                         Local Similarity
ب
                                                                                                                   prevented or treated.
EKQAIKIDKEREEY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EEASKSMESTLESLQSLSAAQMKEVEAVVVAALSGKSSGSAKLETPELPKPGVTPRSEVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QKSKDLEGTMDTVNTVMIA 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EEASKSMESTLESLQSLSAAQMKEVEAVVVAALSGKSSGSAKLETPELPKPGVTPRSEVI
                                                                                                                                                                                                                            5
                                               14;
                                                                                                                                                                                                                         Page 34; 35pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard;
                                                                                             14
                                                                                                                                                                                                                                                                                                                      Matthews
                                               Conservative
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                                                                                              AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide; 14
                                                       2.8%;
                                                                                                                                                                                                                                                                                                                      RC
                                                                                                                                                                                                                          English.
                                                         .0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         epitope
                                              0,
                                                       Score 14;
Pred. No.
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                                              Mismatches
                                                       DB 21; 1
                                                                   Length 14;
                                                                                                                                                                                                                                                            atherosclerosis,
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                                            0,
                                            Gaps
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AAB08336 ID AAB( XX RESULT

AAB08336

standard;

Peptide;

14

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11

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RESULT 8
AAB08323
ID AAB0
XX
AC AAB0
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AC AAB0
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DT 04-D
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20-SEP-1994;
28-APR-1995;
28-APR-1995;
28-APR-1995;
28-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polypeptide antigen, polypeptide A. C. pneumoniae strain YK41 was cultured and genomic DNA extracted to prep. a lambda gtll DNA library. The library was then screened with an anti-YK41 monoclonal antibody (MAD), which was prepd. by fusing spleen cells from a mouse infected with YK41 with myeloma PJNS1/1-Ag4-1 to produce a MAD expressing hydridoma. The DNA obtd. was then fused with the expression vector pADA431 to give pCPNS33alpha. The plasmid was used to transform an E. coli host, which was cultured to give the antigenic polypeptide, polypeptide A. Polypeptide A and primers and probes derived from its DNA can be used in assays for the detection of polypeptide A antibodies and DNA, respectively, useful in the diagnosis of C. pneumoniae infection.
 Amino acid sequence of a Chlamydia pneumoniae His-tagged protein.
                            04-DEC-2000
                                                        AAB08323;
                                                                                AAB08323 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is a variant of the C. pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Pages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HITB ) HITACHI CHEM CO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1996-188399/19.
DB; AAT14613.
                                                                                                                                                      QKSKDLEGTMDTVNTVMIA
                                                                                                                                                                    QKSKDLEGTMDTVNTVMIA
                                                                                                                                                                                                                                                                                                                                   ASGKDKTSSTTKTETAPQQGVAAGKESSESQKAGADTGVSGAAATTASNTATKIAMQTSI 123
                                                                                                                                                                                                                                                                                                                                                                           MSISSSSGPDNQKNIMSQVLTSTPQGVPQQDKLSGNETKQIQQTRQGKNTEMESDATIAG
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                                                                                                                                                                                                                                                                EEASKSMESTLESLQSLSAAQMKEVEAVVVAALSGKSSGSAKLETPELPKPGVTPRSEVI 183
                                                                                                                                                                                                           EIGLALAKAIQTLGEATKSALSNYASTQAQADQTNKLGLEKQAIKIDKEREEYQEMKAAE
                                                                                                                                                                                                                                    EIGLALAKAIQTLGEATKSALSNYASTQAQADQTNKLGLEKQAIKIDKEREEYQEMKAAE 243
                                                                                                                                                                                                                                                                                                                      {\tt ASGKDKTSSTTKTETAPQQGVAAGKESSESQKAGADTGVSGAAATTASNTATKIAMQTSI~120}
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         271
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                           (first entry)
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94JP-0224711.
95JP-0106006.
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95JP-0106009.
95JP-0106010.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               52.2%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pneumoniae antigen and antibodies to it dassay of C. pneumoniae e.g. in clinical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 271;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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RESULT 9
AAR94585
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                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 259
                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a His-tagged Chlamydia pneumoniae protein. The protein, immunogenic fragments of it, nucleotide sequences encoding it, or inhibitor specific against it are used to manufacturing a medicament for the treatment of infection due to C. pneumoniae. An antibody specific against the protein can diagnose a C. pneumoniae infection. C. pneumoniae infection can be prevented. Artherosclerosis, including coronary atherosclerosis, caused by C. pneumoniae can also be prevented or treated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New Chlamydia pneumoniae protein of 496 amino acids preventing and treating C. pneumoniae infection and including coronary atherosclerosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           coronary atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chlamydia pneumoniae protein; infection; artherosclerosis;
                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example; Page 31-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Burnie JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cleavage-site
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                                                             AAEQKSKDLEGTMDTVNTV 259
                                                                                                                EVIEIGLALAKAIQTLGEATKSALSNYASTQAQADQTNKLGLEKQAIKIDKEREEYQEMK
                                                                                                                                                                                                 DTNMSISSSGPDNQKNIMSQVLTSTPQGVPQQDKLSGNETKQIQQTRQGKNTEMESDAT
                                                                                                                                                                TSIEEASKSMESTLESLQSLSAAQMKEVEAVVVAALSGKSSGSAKLETPELPKPGVTPRS
                                                                                                                                                                                                                                                 AAEQKSKDLEGTMDTVNTV
                                                                                                 EVIEIGLALAKAIQTLGEATKSALSNYASTQAQADQTNKLGLEKQAIKIDKEREEYQEMK
                                                                                                                                                TSIEEASKSMESTLESLQSLSAAQMKEVEAVVVAALSGKSSGSAKLETPELPKPGVTPRS
                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                     302
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                                                                                                                                                                                                                                                                                                 52.2%; Score 259; DB 21; llarity 100.0%; Pred. No. 2.7e-222; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                     AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "S-tag and thrombin 292..302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35pp;
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                                                 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cleavage site'
                                                                                                                                                                                                                                                                                                                             Length 302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for diagnosing, atherosclerosis,
                                                                                                                                                                                                                                                                                                    0;
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ΧIJ

AAR94585 standard;

Protein;

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RESULT 6
AAW01743
ID AAW0
XX
AC AAW0
AC AAW0
DT 22-A
XX
DE C. p
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Best Local Sin
Matches 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is the C. pneumoniae polypeptide antigen C polypeptide A clone, 53-3S. C. pneumoniae strain YK41 was C cultured and genomic DNA extracted to prep. a lambda gtll DNA it cultured and genomic DNA extracted to prep. a lambda gtll DNA it cultured and genomic DNA extracted to prep. a lambda gtll DNA it cultured and genomic DNA extracted with an anti-YK41 monoclonal antibody (MAb), which was prepd. by fusing spleen cells from a mouse infected with YK41 with myeloma P3/NSI/1-Ay4-1 to produce a MAb expressing hydridoma. The DNA obtd. was then fused with the expression vector pADA431 to give pCPN533alpha. The plasmid was used to transform an E. coli host, which was cultured to give the antigenic polypeptide, polypeptide A. Polypeptide A and primers and probes derived from its DNA can be used in assays for the detection of polypeptide A antibodies and DNA, respectively, useful in the diagnosis of C. pneumoniae infection.
                 C. pneumoniae 53 kDa
                                         22-APR-1997
                                                               AAW01743;
                                                                                    AAW01743 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-APR-1995;
20-SEP-1994;
28-APR-1995;
28-APR-1995;
28-APR-1995;
28-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant Chlamydia
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                                                                                                                                                                                       EIGLALAKAIQTLGEATKSALSNYASTQAQADQTNKLGLEKQAIKIDKEREEYQEMKAAE
                                                                                                                                              OKSKDLEGTMDTVNTVMIA
                                                                                                                                                                                                                                   EEASKSMESTLESLQSLSAAQMKEVEAVVVAALSGKSSGSAKLETPELPKPGVTPRSEVI
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                                                                                                                                                                                                                                                                                                                                                                            h 52.2%; Si
Similarity 100.0%; I
59; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    detection and
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                                       (first
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95JP-0106006.
95JP-0106008.
95JP-0106009.
95JP-0106010.
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               antigen
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                                                                                     259
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Matches 259
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W09609320-A1
                                Chlamydia pneumoniae
                                                                                                Polypeptide antigen; p
pCPN533alpha; primer;
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                                                                                 infection;
                                                                                                                                                                                                            07-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The protein is that of the Chlamydia pneumoniae 53 kDa antigen. A method for the detection and determination of anti-C. pneumoniae antibodies in a sample comprises using at least 5 consecutive amino acids of the polypeptide C 73 kDa antigen (AAW01742).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Detection and determination of anti-Chlamydia pneumoniae antibody using the polypeptide {\tt C} as the antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1997-056178/06
N-PSDB; AAT59311.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HITB ) HITACHI CHEM
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                                                                                                                                                     pneumoniae polypeptide antigen (polypeptide A) variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 MSISSSSGPDNQKNIMSQVLTSTPQGVPQQDKLSGNETKQIQQTRQGKNTEMESDATIAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EIGLALAKAIQTLGEATKSALSNYASTQAQADQTNKLGLEKQAIKIDKEREEYQEMKAAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EIGLALAKAIQTLGEATKSALSNYASTQAQADQTNKLGLEKQAIKIDKEREEYQEMXAAE
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59; Conservative
                                                                               variant.
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                                                                                                                                                                                                     entry)
                                                                                       polypeptide A; strain YK41; plasmid; probe;
; assay; detection; antibody; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.2%; Score 259; DB 18; 100.0%; Pred. No. 2.4e-222; tive 0; Mismatches 0;
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                                                                                                                28-APR-1995;
20-SEP-1994;
28-APR-1995;
                                                                                                                                                                                                               20-SEP-1995;
                                                                                                                                                                                                                                                           28-MAR-1996.
                                                                                                                                                                                                                                                                                                       WO9609320-A1
                                                                                                                                                                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polypeptide antigen; polypeptide A; strain YK41; plasmid; pr
PCPN533alpha; primer; assay; detection; antibody; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chlamydia pneumoniae polypeptide antigen (polypeptide A).
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(HITB)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VAQFQKEVGKLQAAADMISMFTQFWQQASKIASKQTGESNEMTQKATKLGAQILKAYAAI 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GISKVFAKGTQMIAKNFPKLSKVISSLTSKWVTVGVGVVVAAPALGKGIMQMQLSEMQQN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAATTVATQITVQAVVQAVKQAVITAVRQAITAAIKAAVKSGIKAFIKTLVKAIAKAISK
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                                           95JP-0106011.
94JP-0224711.
95JP-0106006.
95JP-0106008.
95JP-0106009.
95JP-0106010.
                                                                                                                                                                                                               95WO-JP01896
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entry)
                                                                                                                                                                                                                                                                                                                                                     "claimed N-terminal fragment"
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is the C. pneumoniae polypeptide antigen, polypeptide A. C. pneumoniae strain YK41 was cultured and genomic DNA extracted to prep. a lambda gtll DNA library. The library was then screened with an anti-YK41 monoclonal antibody (MAb), which was prepd. by fusing spleen cells from a mouse infected with YK41 with myeloma P3/NS1/1-Ag4-1 to produce a MAb expressing hydridoma. The DNA obtd. was then fused with the expression vector pADA431 to give pCPN533alpha. The plasmid was used to transform an E. coli host, which was cultured to give the antigenic polypeptide, polypeptide A. molypeptide A and primers and probes derived from its DNA can be used in assays for the detection of polypeptide A antibodies and DNA, respectively, useful in the diagnosis of antibodies and DNA, respectively, useful in the diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant Chlamydia used for detection and
                                                                         Chlamydia pneumoniae
                                                                                                                         Polypeptide antigen; polypeptide A; strain YK41; plasmid; probe; pCPN533alpha; primer; assay; detection; antibody; diagnosis;
                                                                                                                                                                                                      11-NOV-1996
                                                                                                                                                                                                                                                                     AAR94586 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Pages 60-64; 128pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Izutsu H,
                28-MAR-1996
                                               WO9609320-A1
                                                                                                            infection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MSISSSSGPDNQKNIMSQVLTSTPQGVPQQDKLSGNETKQIQQTRQGKNTEMESDATIAG
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DB; AAT14612.
                                                                                                                                                                                                                                                                                                                                                                              QKSKDLEGTMDTVNTVMIAVSVAITVISIVAAIFTCGAGLAGLAA 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ASGKDKTSSTTKTETAPQQGVAAGKESSESQKAGADTGVSGAAATTASNTATKIAMQTSI 123
                                                                                                                                                                                                                                                                                                                                              EIGLALAKAIQTLGEATKSALSNYASTQAQADQTNKLGLEKQAIKIDKEREEYQEMKAAE
                                                                                                                                                                                                                                                                                                                                                                                                                                              EIGLALAKAIQTLGEATKSALSNYASTQAQADQTNKLGLEKQAIKIDKEREEYQEMKAAE 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EEASKSMESTLESLQSLSAAQMKEVEAVVVAALSGKSSGSAKLETPELPKPGVTPRSEVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ASGKDKTSSTTKTETAPQQGVAAGKESSESQKAGADTGVSGAAATTASNTATKIAMQTSI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MSISSSSGPDNQKNIMSQVLTSTPQGVPQQDKLSGNETKQIQQTRQGKNTEMESDATIAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                            clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                     (first entry)
                                                                                                                                                                       polypeptide antigen (polypeptide A) clone 53-3S.
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                                                                                                                                                                                                                                                                      Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Obara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 b; Score 285; DB
b; Pred. No. 2.8
0; Mismatches
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                                                                                                                                                                                                                                                                     A
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2.8e-245;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 488;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        especially where the vector directs the expression epitope of C. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY34584-Y35879 represent the proteins encoded by all the open reading frames in the complete genome (see AAX91990) of Chlamydia pneumoniae. C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Griffais
          421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page 1223-1224; Disclosure; 1912pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome sequence of Chlamydia pneumoniae
                                                421
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ISKGISKVFAKGTQMIAKNFPKLSKVISSLTSKWVTVGVGVVVAAPALGKGIMQMQLSEM
                                                                                                                                                                                 AGAAAATTVATQITVQAVVQAVKQAVITAVRQAITAAIKAAVKSGIKAFIKTLVKAIAKA
                                                                                                                                                                                                                                                        AAEQKSKDLEGTMDTVNTVMIAVSVAITVISIVAAIFTCGAGLAGLAAGAAVGAAAAGGA
                                                                                                                                                                                                                                                                                                                  EVIETGLALAKATQTLGEATKSALSNYASTQAQADQTNKLGLEKQATKIDKEREEYQEMK
                                                                                                                                                                                                                                                                                                                                        EVIEIGLALAKAIQTLGEATKSALSNYASTQAQADQTNKLGLEKQAIKIDKEREEYQEMK 240
                                                                                                                                                                                                                                                                                                                                                                                                                                TSIEEASKSMESTLESLQSLSAAQMKEVEAVVVAALSGKSSGSAKLETPELPKPGVTPRS
                                                                             ISKGISKVFAKGTQMIAKNFPKLSKVISSLTSKWVTVGVGVVVAAPALGKGIMQMQLSEM
                                                                                                                                                         AGAAAATTVATQITVQAVVQAVKQAVITAVRQAITAAIKAAVKSGIKAFIKTLVKAIAKA
                                                                                                                                                                                                                                      AAEQKSKDLEGTMDTVNTVMIAVSVAITVISIVAAIFTCGAGLAGLAAGAAVGAAAAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IAGASGKDKTSSTTKTETAPQQGVAAGKESSESQKAGADTGVSGAAATTASNTATKIAMQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          487;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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97FR-0014673.
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100.0%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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SQ XXX

Вb QΥ В δÃ B Qy Дb δÃ В Qγ В Qy DЬ Qy В Qy

Query Match Best Local Similarity

99

. 83

Score Pred.

386; No. 0;

DB 17;

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RESULT 3
AAR94584
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                  p3/NSI/1-Ag4-1 to produce a MAb expressing hydridoma. The DNA obtd. was then fused with DHFR DNA and the expression vector pADA431 to give pCPNS33T. The plasmid was used to transform an E. coli host, which was cultured to give the antigenic polypeptide fusion protein, polypeptide B. Polypeptide B and primers and probes derived from its DNA can be used in assays for the detection of antigenic polypeptide antibodies and DNA, respectively, useful in the diagnosis of C. pneumoniae infection.
Sequence
                                                                                                                          C. pneumoniae polypeptide antigen fusion protein, polypeptide B. c. pneumoniae strain YK41 was cultured and genomic DNA extracted to prep. a lambda gtll DNA library. The library was then screened with an anti-YK41 monoclonal antibody (WAb), which was prepd. by fusing spleen cells from a mouse infected with YK41 with myeloma
                                                                                                                                                                                               The present sequence is the dihydrofolate reductase (DHFR)/
                                                                                                                                                                                                                        Claim 22; Pages 97-103; 128pp; Japanese
                                                                                                                                                                                                                                                             Recombinant Chlamydia pneumoniae antigen and antibodies to it used for detection and assay of C. pneumoniae e.g. in clinical
                                                                                                                                                                                                                                                                                                          N-PSDB; AAT14618
                                                                                                                                                                                                                                                                                                                                                                                                     28-APR-1995;
28-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                            28-APR-1995;
28-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-APR-1995;
20-SEP-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polypeptide antigen; polypeptide B; strain yK41; pCPN533T; primer; assay; detection; antibody; dia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DHFR/C. pneumoniae antigen fusion protein (polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-NOV-1996
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                                                                                                                                                                                                                                                                                                                                                Matsumoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fusion protein; dihydrofolate reductase; DHFR; pneumoniae.
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 AΑ;
                                                                                                                                                                                                                                                                                                                                                                                                  95JP-0106011.
94JP-0224711.
95JP-0106006.
95JP-0106008.
95JP-0106009.
95JP-0106010.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95WO-JP01896
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/label= dihydrofolate reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= C. pneumoniae antigen
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Burnie JP,
                                      10-AUG-2000
                                              WO200046359-A2
                                                      Chlamydia pneumoniae
                                                               coronary
                                                                   Chlamydia
                                                                                    04 - DEC - 2000
                             28-JAN-2000;
                                                                          Amino acid sequence of a Chlamydia pneumoniae protein
                                                                                                    AAB08322 standard;
            (NEUT-) NEUTEC PHARMA PLC
                                                                                                                                       a pneumoniae protein; infection; artherosclerosis, atherosclerosis.
    Matthews RC;
                             2000WO-GB00237
                                                                                   (first
                                                                                                                                       99GB-0002555
                                                                                                    Protein;
                                                                                   entry)
                                                                                                                                       496
                                                                                                                                                  AAU11788
AAB66314
AAR66318
AAY56352
ABB04546
AAM43445
ABB28775
ABB28775
ABB33962
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ABB134726
ABB134726
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AAM54726
AAM54726
AAM54727119
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AAE15591
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AAE157610
AAR457611
AAW06201
AAW33400
ABB30513
AAU09054
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AAR356787
AAR36789
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AAR80170
AAW17683
AAW170279
AAB14996
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AAR45762
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AAW68413
                                                                                                                          ALIGNMENTS
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                                                                                                                                                                                                                                      Wild-type human Fc
Mutant human Fcgam
Hamster PrP peptide
Murine PrP (HuPrP)
                                                                                                                                                  Peptide #1420 (Peptide #1456 (Peptide #1393)
                                                                                                                                                                                                    Silk spider spidro
Silk fibre forming
P acnes linoleate
                                                                                                                                                                                                                                                                Hamster Prp peptide
Murine Prp peptide
Human Prp peptide
                                                                                                                                                                                                                                                                            Prion protein pept
Generic peptide se
Amino acids 109-14
                                                                                                                                          Human peptide
C-terminal por
                                                                                                                                                               Human brain expres
                                                                                                                                                                        Peptide #1468
Protein #1400
                                                                                                                                                                                   Hepatitis C capsid
Scorpion toxin-rel
                                                                                                                                                                                            MiSPI-derived poly
Bacillus subtilis
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Peptide #3164 enco
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Spider dragline va
                                                                                                                                                                                                                                  Murine PrP mutant
                                                                                                                                                                                                                                                            Mutant murine Prp
                                                                                                                                                                                                                                                                                         Prion protein
MiSP1-derived
                                                                                                                                                                                                                                                                                                 Prion protein
                                                                                                                                      BS106 synthetic
                                                                                                                                                                                Peptide #1426
                                                                                                                                                                                                                                                                                                      Tyr-hBNP.
                                                                                                                                                                                                                                                                                                               Human mature
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RESULT 2
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents a Chlamydia pneumoniae protein. The protein, immunogenic fragments of it, nucleotide sequences encoding it, or inhibitor specific against it are used to manufacturing a medicament for the treatment of infection due to C. pneumoniae. An antibody specific against the protein can diagnose a C. pneumoniae infection. C. pneumoniae infection can be prevented. Artherosclerosis, including coronary atherosclerosis, caused by C. pneumoniae can also
                                                         13-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 30-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            including coronary atherosclerosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New Chlamydia pneumoniae protein of 496 amino acids for diagnosing, preventing and treating C. pneumoniae infection and atherosclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAA63621.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-543485/49
                               Amino acid sequence of a Chlamydia pneumoniae protein.
                                                                                 AAY35449;
                                                                                                          AMT 35449 St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          be prevented or treated.
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                                                                                                                                                                                 AAISGAIAGAHKTNNF 496
                                                                                                                                                                                                                               QQNVAQFQKEVGKLQAAADMISMFTQFWQQASKIASKQTGESNEMTQKATKLGAQILKAY
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                                                                                                                                                                      AAISGAIAGAHKTNNF
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                                                         (first
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                                                         entry)
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Pred. No. 0;
0; Mismatches
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Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis;

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2222211114443;	
AAR62530  AAW16411  AAY69439  AAW191710  ABB41243  ABB41243  ABB41243  ABB425842  ABB26585  AAW62109  AAW74917  ABB467027  ABB46719  ABB75912  ABB77912  ABB79118  AAW79119  AAW79110  ABB79118  AAW79110  AAW79701	AAB66319 AAW71153 AAW706705 AAB14995 ABB43915 ABB26833 AAW64905 AAW77641 AAW21563 AAW77641 AAW21563 AAW37837 AAB82099 AB646673 AAEL5590
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OM protein - protein search, using sw model

Run on: January 27, 2003, 16:32:30; Search time 31 Seconds (without alignments) 2132.010 Million cell updates/sec

Scoring table: Perfect score: US-09-889-314-2 496 DTNMSISSSSGPDNQKNIMS.....LKAYAAISGAIAGAHKTNNF 496

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Title:

908470 segs, 133250620 residues Gapop 60.0 , Gapext 60.0

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Word size : 0

Total number of hits satisfying chosen parameters: 908470

Minimum DB Maximum DB Minimum seq length: 0 seq length: 2000000000

Post-processing: Listing first 1000 summaries /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:

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356 AlaIleAlaLysAlaIleSerLysGlyIleSerLysValPheAlaLysGlyThrGlnMet 375
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                                                                                                                                               AlaValValGlnAlaValLysGlnAlaVal----IleThrAlaValArgGlnAlaIleThr 335
                                                                                                                                                                                                                                                GlnGluMetLysAlaAlaGluGlnLysSerLysAspLeuGluGlyThrMetAspThrVal
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                                                                             AlaAlaIleLysAlaAlaValLysSerGlyIleLysAlaPheIleLysThrLeuValLys 355
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                                                                                                                                                                                     -----ATGGTGGCCGATGAAATT-----
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VΩ	Db	Qy	Qу ДЪ	Фр	US-0	Alignme Pred. N Score: Percent Best Lo Query M DB:	BASE ORIG	REFERENC AUTHOR TITLE JOURNA FEATURES	SOURCE	RESULT AR08244 LOCUS DEFINIT ACCESSION VERSION KEYWORD	Дb	QУ	Оу	Qy Db	Дb	Qy	Оу	Оy	Db	Qy	DЪ
88 1	1019	68	968	908	9-889-	ment No.: : nt Si Local Matc	COUNT	H E RH	23	RESULT 45 AR082441 LOCUS DEFINITION ACCESSION VERSION KEYWORDS	2114	479	462 2054	450 1994	1937	430	410 1889	396 1829	1769	376	1724
8 LysGluSerSerGluSerGlnLysAlaGlyAlaAspThrGlyVal 102	9AGACGGATACCGCCAAGAGTGTTTATGACGCTGCGA	8 AspLysThrSerSerThrThrLysThrGluThrAlaProGlnGlnGlyValAlaP	8 ArgGlnGlyLysAsnThrGluMetGluSerAspAlaThrIleAlaGlyAlaSerGlyLys 67		9	nt Scores: 0.00316 Length: 3622 218.50 Matches: 116 Similarity: 41.02% Conservative: 85 cal Similarity: 23.67% Mismatches: 182 stch: 9.22% Indels: 107 Gaps: 20	INT 1049 a 759 c 1008 g 806 t	א פי א	23	45 1 AR082441 3622 bp DNA linear PAT 31-AUG ION Sequence 7 from patent US 5972899. ON AR082441 GI:10009167 AR082441.1 GI:10009167	ACCGCAGCCCAGTCAG	ø	2 SerAsnGluMetThrGlnLysAlaThrLysLeuGlyAlaGlnTleLeuLys 47         ::::: 4 AGTAAAGAGCTGGTAGGTAATACCCTAAATAAAGTGGCGTTGGGCATGGAAGTCACGAAT 21	50 Gln	7 AACGTGCTGAAACAGTTGGCGCAAAAACGGCAGCAAACTCTTTACCCAGGGGATGCAA 1	0 GluValGlyLysLeuGlnAlaAlaAlaAspMetIleSerMetPheThrGlnPheTrpGln	10 LysGlyIleMetGlnMetGlnLeuSerGluMetGlnGlnAsnValAlaGlnPheGlnLys 429 ::: ::: ::: ::: 89 AACGCGCTGAGCAAAATGATGGGCGAAACGATTAAGAAGTTGGTGCCT 193	96 ThrValGlyValGlyValValValAlaAlaProAlaLeuGly 4	6	6 IleAlaLysAsnPheProLysLeuSerLysValIleSerSerLeuThrS	24 CTGATTGGCAAGGCGATTACCAAAGCGCTGGAAGGATTAGGCGTC 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGTATTACTAGCGGTCTGGGTAATGTAGGTAGCAAGATGGCCTGCAAACGAATGCCTTA
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    Kaniga,K., Tucker,S., Trollinger,D. and Galan,J.E. Homologs of the Shigella IpaB and IpaC invasins are required Salmonella typhianurium entry into cultured epithelial cells J. Bacteriol. 177 (14), 3965-3971 (1995)
                                                                                                                              Salmonella typhimurium.
Salmonella typhimurium
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                      STU25631 3622 bp DNA linear I Salmonella typhimurium invasin homologs SicA (sicA), and SipC (sipC) genes, complete cds. U25631
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                                                                                                               Salmonella.
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Direct Submission
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VLKTVINKVSLNIYILSKRLESVESDIRLEQNYMDITRIDSAQDADDGRSDYEELGHG
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                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
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614 c 847 g 683 t
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180562 CAGGCGATGATTGAGTCACAAAAAGAGATGGGGATTCAGGTATCGAAAGAATTCCAGACG

180503

ArgGlnGlyLysAsnThrGluMetGluSerAspAlaThrIleAlaGlyAlaSerGlyLys

GAGGCTCAGGAGGCGACGGATCTCTATGAAGCCAGCATCAAA 180452

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88

LysGluSerSerGluSerGlnLysAla -----

180502

GCTCTGGGA-----

48

8

AspLysThrSerSerThrThrLysThrGluThrAlaProGlnGlnGlyValAlaAlaGly 87

AAGACGGATACCGCCAAGAGTGTTTATGACGCTGCGGCC

180413

GlyAlaAspThrGlyVal 102

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Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                              6651.
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SEFTALDVTLDIAPFDGDNESRLAVRPYPHQLEEWVEMKNGDRCLFRPILPEDEPQLR
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to PSS_ECOLI (451 aa),
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41.02%
23.67%
9.31%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to entry PF00583 Acetyltransf, (GNAT) family, score 59.00, E-value
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          coli pssA (PSS_ECOLI);
94% identity in 451 aa (
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GGGAAAGTCCTCGGCGCGCTG------CTAACCATTGTCAGCGTTGTGGCCGCTGTT

AsnThrValMetIleAlaValSerValAlaIleThrValIleSerIleValAlaAlaIle

276

179945

PheThrCysGlyAlaGlyLeuAlaGlyLeuAlaAlaGlyAlaAlaValGlyAlaAlaAla

296

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297

AlaGlyGlyAlaAlaGlyAlaAlaAlaAlaThrThrValAlaThrGlnIleThrValGln

316

179828

----ATGGTGGCCGATGAAATT-----

AlaValValGlnAlaValLysGlnAlaVal---IleThrAlaValArgGlnAlaIleThr

-GTGAAGGCGGCGACGGGGGTGTCGTTTATTCAGCAGGCGCTAAAC 179783

179747

TTTACCGGTGGGGCGAGTCTGGCGCTGGCTGGGGTGGGACTTGCGGTA

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GlnGluMetLysAlaAlaGluGlnLysSerLysAspLeuGluGlyThrMetAspThrVal TTCAACGCCTTGCAGGAAGGGCGTCAGGCG - - - GAGATGGAAAAGAAATCGGCTGAATTC

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---GAGACGCGCAAAGCCGAGGAAACGAACCGCATTATGGGATGTATC

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180154 GATAATCTGTCAAATGTCGCCCGCCTCACTATGCTCATGGCCATGTTTATTGAGATTGTG

GlyGluAlaThrLysSerAlaLeuSerAsnTyrAlaSerThrGlnAlaGlnAlaAspGln

216

180053

180095

180155

180215

180214 ACCAAATTCCAGGGAACGGCTAATGCCGCCTCTCAGAATCAGGTTTCCCCAGGGTGAGCAG

ProArg---SerGluValIleGluIleGlyLeuAlaLeuAlaLysAlaIleGlnThrLeu

GlyLysSerSerGlySerAlaLysLeuGluThrProGluLeuProLysProGlyValThr 177

GCGACGGTTAAAGCAGGCACAGACGCCAAAGCCGAAAGCCGAGAAAGCGGATAACATTCTG

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197

180094

GGCAAAAATACGGAAGAAAGCCTGCAAAACGATCTTGCGCTT---

ThrAsnLysLeuGlyLeuGluLysGlnAlaIleLysIleAspLysGluArgGluGluTyr 236

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AlaGlnMetLys-----

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IleGluGluAlaSerLysSerMetGluSerThrLeuGluSerLeuGlnSerLeuSerAla 142

GTAGAACAGGCCGGAAAAGAAGCGACAGAGGCCGAAAGAGGCCCTTAGATAAGGCCCACGGAT 180275

-----GluValGluAlaValValAlaAlaLeuSer 157

SerGlyAlaAlaAlaThrThrAlaSerAsnThrAlaThrLysIleAlaMetGlnThrSer 122 AAAAAACTGACGCAGGCGCAAAAATAAATTGCAATCGCTGGACCCAGCTGACCCCGGCTAT 180353

----GCG

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180352

GCACAAGCTGAAGCC:

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CDS

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Qy 376    IleAlaLysAsnPheProLysLeuSerLysVallIeSerSerLeuThrSerLysTrpVal 395	.8 GlnGlyValProGlnGlnAspLysLeuSerGlyAsnGluThrLysGlnIleGlnGlnThr 47	LeuSerGlyAsnGluThı	GlnGlnAspLys	8 GlnGlyValPro
		(1-274050)	) x AL627276	9-314-2 (1-496) x AL627276 (1-274050)
Db 179746 CTGATTGGCAAGGCGATTACCAAAGCGCTGGAAGGATTAGGCGTC 17970				
	20	Gaps:	ب	
Qy 356 AlaIleAlaLysAlaIleSerLysGlyIleSerLysValPheAlaLysGlyThrGlnMet 375	107	Indels:	9.31%	ch:
	182	Mismatches:	23.67%	l Similarity:
Db 179782 CCGATTATGGAGCATGTGCTGAAGCCGTTAATGGAG 17974	2: 85	Conservative:	41.028	Similarity: 41.02%
	116	Matches:	220.50	
Qy 336 AlaAlaIleLysAlaAlaValLysSerGlyIleLysAlaPheIleLysThrLeuValLys 355	274050	Length:	0.447	:

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US-09-889-314-2 (1-496) x AL627276

Score:

misc_teature 322. 867 /gene="STY2840" /note="Pfam match to entry PF00315 UNG, Uracil-DNA glycosylase, score 451.20, E-value 9e-132"	/codon_start=1 /trans!_table=11 /trans!_table=11 /product="uracil-DNA glycosylase" /protein_id="CAD05831.1" /protein_id="CAD05831.1" /db_xref="GI:16503806" /db_xref="GI:16503806" /db_xref="GFTREMBL;Q8XGK6" /translation="MATELTHHOVLADEXQQPYEINTLHTVAI ftranslation="MATELTHHOVLADEXQQPYEINTLHTVAI ftranslation="MATELTHHOVLADEXQQPYEINTLHTVAI ftranslation="MATELTHHOVLADEXQQPYEINTLHTVAI ftranslation="MATELTHHOVLADEXQPYEINTLHTVAI ftranslation="MATELTHHOVLADEXQ	/note="ung" 208. 897 /gene="STY2840" /EC_number="3.2.2" /note="Orthologue of E. coli ung (UNG_ECOLI); Fasta hit to UNG_ECOLI (228 aa), 91% identity in 228 aa overlan"	/db_xref="taxon:90370" 197201 /note="possible RBS" gene	Details of S. typhi sequencing at the Sanger Centre are available on the World Wide Web.  (URL, http://www.sanger.ac.uk/Projects/S_typhi/).  FEATURES Cocation/Qualifiers  source 1274050 /organism="Salmonella enterica subsp. enterica serovar Typhi" = "CT18"	PUBMED 1107608  REFERENCE 2 (bases 1 to 274050)  RUTHORS Parkhill,J.  TITLE Direct Submission  JOURNAL Submitted (25-OCT-2001) Submitted on behalf of the Salmonalla sequencing team, Sanger Centre, Wellcome Trust Genome Campus,  Hinxton, Cambridge CB10 1SA, UK  E-mail: parkhill@sanger.ac.uk	Connerton, P., Cronin, A., Davis, P., I Farrar, J., Feltwell, T., Hamlin, N., I Jagels, K., Krogh, A., Larsen, T.S., L., Parry, C., Quall, M., Rutherford, K., Stevens, K., Whitehead, S. and Barrel. Complete genome sequence of a multipenterica serovar Typhi CT18 Nature 413 (6858), 848-852 (2001)	503805  ca subsp. enteri ca subsp. enteri acteria; gamma s actoria; James, K.D an, G., James, K.D an, G. Bangall, K.L	82 ACCGCAGCCCAGTC 42 42 6/c AL627276 ION Salmonella e complete chr ON AL627276 AL5	Qy 479 AlaTyrAlaAlaIleSerGlyAlaIleAla 488
gene 34806140 /gene="STY2844" CDS 34806140 /gene="STY2844"	/rip_ECULI (32 aa), 88% identit (codon_start=1 /codon_start=1 /transl_table=11 /product="conserved hypothetical/product="conserved hypothetical/protein_id="cAbD5834.1" /protein_id="cAbD5834.1" /db_xref="GI:16503809" /db_xref="SPTREMBL:0824J5" /franslation="MYNNAYOLKARERLARAT	). E	ch to -value	/product="thioredoxin 2" /protein_id="CADD5833.1" /db_xref="01:16503808" /db_xref="01:16503808" /db_xref="SPTREMBL:Q824J6" /translation="NMTVCTPHCQAIMRIPGDRIQDAAK /translation="NMTVCTPHCQAIMRIPGDRIQDAAK IDKLIKDDLPVVIDMAPMCGPCRNFAPIFEDVAEERS GIRSIPMIMIEKHGQVVDMLNGAVPKAPFDSWLNEAL" misc_feature 23532670	gene 22542673  /gene="STY2842" /note="txxC; yfiG" /note="txxC; yfiG" 22542673 /gene="STY2842" /note="Orthologue of E. /codon_start=1 /trans1_table=11	AHFGYKGVVVQDAALLESGAAIR SDRGQALFSTTLPEKMYLVLGRE LLAEWWRQNKA* misc_feature complement(10401462) /gene="STY2841" /note="pfam match to en rRNA Methylase family, RBS 2244248 /note="possible RBS"	/transl_table=11 /transl_table=11 /product="putative RNA met /product="cab05832.1" /protein_id="cab05832.1" /db_xref="cst0503807" /db_xref="SpTREMB1:Q8XFT1" /translation="MNDEKHETSWR DGGRRPARDERNQSRDALFQSRDALFQ QRAEETRYVGENACQALFQSRDALFQ ELAKASGTEHHGGVCFLIKKRNGTTV	/note="ps00130 Uraci1-DNA glycosylase complement(10132050)  /gene="syry2841" /note="yfif"  CDS complement(10132050) /gene="syry2841" /note="0yry2841"	<pre>misc_feature 376 .405 /gcne="STY2840"</pre>
	Identity in 226 thetical protein' 5" AERLARATRPFLARGNE NUCRLIADDILPDTAARC AGKPPLFIMLDGTWPER VAIALLDLAGDPEAATS	i YFIP_ECOLI; Fasta hit	PF00085 thiore	/product="thioredoxin 2" /protein_id="CAD05833.1" /protein_id="CAD05833.1" /db_xref="GI:16503808" /db_xref="SPTREMBL:0824J6" /translation="MNTVCTHCQAINRIPGDRLQDAAKCGRCGHELFDGEVINATGET LDKLLKDDLPVVIDFWAPWCGPCRNFAPIFEDVAEERSGKVRFVKVNTEAERELSARF GIRSIPMINIFKHGQVVDMLNGAVPKAPFDSWLNEAL" 2353. 2670	coli yfiG (THI2_ECOLI); Fasta hit 94% identity in 139 aa overlap"	AHFOVKGVVVODAALLESGAAIRTAEGGAEHYQPITGESIUDYLDDERQAGYTVVTTS SDRGQALFSTTLPEKMVLVLGREYDYLPEAAREPDDLCVKINGTGNVESLNVSVATGV LLAEMWRQNKA* (complement(10401462) /gene="STY2841"1462) /note="Pfam match to entry PF00588 SpoU_methylase, SpoU /note="SpoU"methylase, SpoU /note="SpoU"methyl	/transl_table=11 /transl_table=11 /product="putative RNA methyltransferase" /product="putative RNA methyltransferase" /protein_id="CADD5832.1" /protein_id="CADD5832.1" /db_xref="G1:16503807" /db_xref="SpTREMBL:Q8XFT1" /db_xref="SpTREMBL:Q8XFT1" /translation="MNDELKNKSGKVKVMYVRSDDDSDKRTHNPRTGKGGGRPAKSRT /CRAESTAUTORADERNNGSTDFBVLRR /GRAFDARDERNNGSDRDKHETSPWRTVSRAPGDETPEKVDHGGISGKSFIDFBVLRR /RAESTRVGENACQALFOSRPDATURAWFIQSVTPRKFALRWMAANKAYHVVDEA ELAKASGTEHHGGVCFLIKKRNGTTVKQWVKQAADQDCVLALEDVANPHNLGGMMRSC	NA glycosylase signature"  coli yfiF (YFIF_ECOLI); Fasta hit 88% identity in 345 aa overlap"	

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BASE COUNT
ORIGIN
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  123 IleGluGluAlaSerLysSerMetGluSerThrLeuGluSerLeuGlnSerLeuSerAla 142 :::|||:::||| ||| |||
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AACGTGCTGAAA---CAGTTGGCACAAAACGGCAGCAAACTCTTTACCCAGGGGATGCAA 1961
                                               GCACAAGCTGAAGCC----
                                                                 SerGlyAlaAlaAlaThrThrAlaSerAsnThrAlaThrLysIleAlaMetGlnThrSer 122
                                                                                                    AAAAAACTGACGCAGGCGCAAAATAAATTGCAATCGCTGGACCCAGCTGACCCCGGCTAT 1085
                                                                                                                             LysGluSerSerGluSerGlnLysAla--
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                                                                                                                                                                                                                   GCTCTGGGA-----GAGGCTCAGGAGGCGACGGATCTCTATGAAGCCAGCATCAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 5393)
Zychlinsky,A. and Chen,Y.
Apoptosis induced by Shigella IpaB
Patent: US 5972899-A 9 26-OCT-1999;
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Sequence 9 from patent US 5972899.
AR082442 GI:10009168
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450 GlnAlaSerLysIleAlaSerLysGlnThrGlyGlu 461	Qy
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430 GluValGlyLysLeuGlnAlaAlaAlaAspMetIleSerMetPheThrGlnPheTrpGln 449	ОУ
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1797 ATGGTAGCGGTCATTGTGGTGGTCGCAGTTGTCGGGAAAGGCGCGGCGGCGAAACTGGGT 1856	Db
396 ThrValGlyValGlyValValValAlaAlaProAlaLeuGly 409	Оу
1737 GATAAGAAAACGGCAGAGATGGCAGCAGTTGTTGGTGCGATTGTCGCCGCTATTGCC 1796	Db
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TIGGCAAGGCGATTACCAAAGCGCTGGAAGGATTAGGCGTC	Db -
356 AlaIleAlaLysAlaIleSerLysGlyIleSerLysValPheAlaLysGlyThrGlnMet 375	ρy
1656 CCGATTATGGAGCATGTG	Db
336 AlaAlaIleLysAlaAlaValLysSerGlyIleLysAlaPheIleLysThrLeuValLys 355	У
1611GTGAAGGCGGCGACGGGGGTGTCGTTTATTCAGCAGGCGCTAAAC 1655	Db
317 AlavalvalGinAlavalLysGinAlaValIleThrAlavalArgGinAlaIleThr 335	Qy
1593 1610	рb
297 AlaGlyGlyAlaAlaGlyAlaAlaAlaAlaThrThrValAlaThrGlnIleThrValGln 316	Qy
1545 TTTACCGGTGGGGCGAGTCTGGCGCTGGCTGCGGTGGGACTTGCGGTA 1592	Db
277 PheThrCysGlyAlaGlyLeuAlaGlyLeuAlaAlaGlyAlaAlaValGlyAlaAlaAla 296	Qy
1494 GGGAAAGTCCTCGGCGCGCTGCTAACCATTGTCAGCGTTGTGGCCGCTGTT 1544	מם
257 AsnThrValMetIleAlaValSerValAlaIleThrValIleSerIleValAlaAlaIle 276	Qy
1443 CAGGAAGAGACGCGCAAAGCCGAGGAAACGAACCGCATTATGGGATGTATC 1493	Db
237 GlnGluMetLysAlaAlaGluGlnLysSerLysAspLeuGluGlyThrMetAspThrVal 256	Qy
1386 TTCAACGCCTTGCAGGAAGGGCGTCAGGCGGAGATGGAAAAGAAATCGGCTGAATTC 1442	Db
217 ThrAsnLysLeuGlyLeuGluLysGlnAlaIleLysIleAspLysGluArgGluGluTyr 236	Qy
1344 GGCAAAAATACGGAAGAAAGCCTGCAAAACGATCTTGCGCTT 1385	Db
197 GlyGluAlaThrLysSerAlaLeuSerAsnTyrAlaSerThrGlnAlaGlnAlaAspGln 216	ОУ
1284 GATAATCTGTCAAATGTCGCCCGCCTCACTATGCTCATGGCCCATGTTTATTGAGATTGTG 1343	Db
178 ProArgSerGluValIleGluIleGlyLeuAlaLeuAlaLySAlaIleGlnThrLeu 196	Qy
1224 ACCAAATTCCAGGGAACGGCTAATGCCGCCTCTCAGAATCAGGTTTCCCAGGGTGAGCAG 1283	Db
158 GlyLysSerSerGlySerAlaLysLeuGluThrProGluLeuProLysProGlyValThr 177	Qy
1164 GCGACGGTTAAAGCAGGCACAGACGCCAAAGCCGAAAGCCGAGAAAGCGGATAACATTCTG 1223	Db
143 AlaGlnMetLysGluValGluAlaValValValAlaAlaLeuSer 157	Qу
1104 GTAGAACAGGCCGGAAAAGAAGCGACAGAGGCCGAAAGAGGCCCTTAGATAAGGCCACGGAT 1163	Дb

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                                                                                                                                                     US-09-889-314-2 (1-496) x STSIPGNS
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                                                                                                                                                                                                                                                                                          Score:
                                                                                                                                                                                                                                                                                                                                                                                 ORIGIN
                                                                                                                                                                                                                                                                                                                 Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
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                                                                                                                                                                                                                                                                                                                 No.:
                                                                  876
                         48
                                                                                                              28
                                                                CAGGCGATGATTGAGTCACAAAAAGAGATGGGGATTCAGGTATCGAAAGAATTCCAGACG
                                                                                                                                                                                                                                                                                                                                      Scores:
GlnGlyValProGlnGlnAspLysLeuSerGlyAsnGluThrLysGlnIleGlnGlnThr
                                                                                                                                                                                                                                              Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                        1584
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/transl_table=11
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LNATSDSPEAKTILMKVGAEYTAQIIKDGLKEKSAFGPWLPETKKAEAKLENLEKQLL
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2352. .3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="sptrembl:Q56136"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GIKNSNKQISPEHQAILSKRLESVESDIRLEQNTMDMTRIDARKMOMTGDLIMKNSVT
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3651. . 4670
                                                                                                                                                                                                                                                                                                                                                                                                                           VEALDMCHQKLTQEQGT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                DIIKNNTGGELSKLSTNLVMQEVMPYIASCIEHNFGCTLDPLTRSSLTQLVDKAAAKA
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3651. .4670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AELQKAMSSAVQQNADASRFILRQSRA" 2352. .3581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELDNAKYQAWQSGFKAQEENLKTTLQTLTQKYSNANSLYDNLVKVLSST1SSSLETAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEGLGVDKKTAEMAGSIVGAIVAAIAMVAVIVVVAVVGKGAAAKLGNALSKMMGETIK
KLVPNVLKQLAQNGSKLFTQGMQRITSGLGNVGSKMGLQTNALSKELVGNTLNKVALG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FTGGASLALAAVGLAVMVADEIVKAATGVSFIQQALNPIMEHVLKPLMELIGKAITKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NDLALFNALQEGRQAEMEKKSAEFQEETRKAEETNRIMGCIGKVLGALLTIVSVVAAV
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220.50
41.02%
23.67%
9.31%
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Matches:
Conservative:
Mismatches:
Indels:
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  1797
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ATGGTAGCGGTCATTGTGGTGGTCGCAGTTGTCGGGAAAGGCGCGGCGGCGAAACTGGGT 1856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAGGAA--
                                       ThrValGlyValGlyValValVal-----
                                                                                                                                                                                                 AlaIleAlaLysAlaIleSerLysGlyIleSerLysValPheAlaLysGlyThrGlnMet 375
                                                                                                                                                                                                                                                                                                                                                                                                  AlaValValGlnAlaValLysGlnAlaVal---IleThrAlaValArgGlnAlaIleThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTTACCGGTGGGGCGAGTCTGGCGCTGGCTGGGGACTTGCGGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PheThrCysGlyAlaGlyLeuAlaGlyLeuAlaAlaGlyAlaAlaValGlyAlaAlaAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGAAAGTCCTCGGCGCGCTG-------CTAACCATTGTCAGCGTTGTGGCCGCTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GlnGluMetLysAlaAlaGluGlnLysSerLysAspLeuGluGlyThrMetAspThrVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTCAACGCCTTGCAGGAAGGGCGTCAGGCG----GAGATGGAAAAGAAATCGGCTGAATTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GATAATCTGTCAAATGTCGCCCGCCTCACTATGCTCATGGCCATGTTTATTGAGATTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTAGAACAGGCCGGAAAAGAAGCGACAGAGGCCGAAAGAGGCCCTTAGATAAGGCCACGGAT 1163
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                                                                                     AlaAlaIleLysAlaAlaValLysSerGlyIleLysAlaPheIleLysThrLeuValLys 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AlaGlyGlyAlaAlaGlyAlaAlaAlaAlaThrThrValAlaThrGlnIleThrValGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AsnThrValMetIleAlaValSerValAlaIleThrValIleSerIleValAlaAlaIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ThrasnLysLeuGlyLeuGluLysGlnalaIleLysIleAspLysGluArgGluGluTyr 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCAAATTCCAGGGAACGGCTAATGCCGCCTCTCAGAATCAGGTTTCCCCAGGGTGAGCAG 1283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GlyLysSerSerGlySerAlaLysLeuGluThrProGluLeuProLysProGlyValThr 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCGACGGTTAAAGCAGGCACAGACGCCAAAGCGAAAGCCGAGAAAGCGGATAACATTCTG 1223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAAAAAACTGACGCAGGCGCAAAATAAATTGCAATCGCTGGACCCCAGCTGACCCCGGCTAT 1085
                                                                                                                            IleAlaLysAsnPheProLysLeuSerLysValIleSerSerLeuThrSerLysTrpVal 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SerGlyAlaAlaAhrThrAlaSerAsnThrAlaThrLysIleAlaMetGlnThrSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LysGluSerSerGluSerGlnLysAla---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -SerGluValIleGluIleGlyLeuAlaLeuAlaLysAlaIleGlnThrLeu 196
                                                                                                                                                                                                                                                                                                                                                        -GTGAAGGCGGCGACGGGGGGGGTGTCGTTTATTCAGCAGGCGCTAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -GAGACGCGCAAAGCCGAGGAAACGAACCGCATTATGGGATGTATC
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                                         ----AlaAlaProAlaLeuGly 409
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256

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1343

1796

1655 335

1691

316 1592 296 1544

431	1 yIlemetGlnMetGlnLeuSerGluMetGlnGlnAsnValAlaGlnPheGlnLysGluVa	41	<b>∳</b> &
173856	S AGCAGCAGTAGCAACAGAAATCACAGTAATAACAGTAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCA	17391	g
411		401	οy
400 173916	11 oLysLeuSerLysValIleSerSerLeuThrSerLysTrpValThrValGlyValGly :::	38 17397	οу
381 173976	2 rLysGlyIleSerLysValPheAlaLysGlyThrGlnMetIleAlaLysAsnPhePr	, 362 5 174029	da Vo
362 174030	3 SSerGlyIleLysAlaPheIleLysThrLeuValLysAlaIleAlaLysAlaIleSe :::    ::                    :: 9 AGCAACAATAAGAGCAGCAACAACAACAACAACAATAAC	343 174089	οу
343 174090	3 SGlnAlaValIleThrAlaValArgGlnAlaIleThrAlaAlaIleLySAlaAlaValLy	, 323 ) 174149	dq VQ
323 174150	7 aValValGlnAlaValLy ::: ::: ::: ::: ::: ::: ::: ::: ::: :	317 174209	Оy
317 174210	7 aGlyGlyAlaAlaGlyAlaAlaAlaAlaThrThrValAlaThrGlnIleThrValGlnAl	29 17426	d Vo
297 174270	7 eThrCysGlyAlaGlyLeuAlaGlyLeuAlaAlaGlyAlaAlaValGlyAlaAlaAlaAlaIIII	27 17432	Db VQ
277 174330	7 nThrvalMetIleAlavalServalAlaIleThrvalIleSerIlevalAlaAlaIlePh	25 17438	Оу
257 174387	7 nGluMetLysAlaAlaGluGlnLysSerLysAspLeuGluGlyThrMetAspThrValAs	23 17443	dd Vo
237 174437	7 rAsnLysLeuGlyLeuGluLysGlnAlaIleLysIleAspLysGluArgGluGluTyrGl	217	Ф
217 174474	7 yGluAlaThrLysSerAlaLeuSerAsnTyrAlaSerThrGlnAlaGlnAlaAspGlnTh	19 17453	Оy
197 174534	7 rProArgSerGluValIleGl     2 AACAGTATCA	17 17457	da Vo
177 174573	7 rGlyLysSerSerGlySerAlaLysLeuGluThrProGluLeuProLysProGlyValTh ::::::::::::::::::::::::::::::::::::	15 17463	ф
157 174633	UGlnSerLeuSerAlaAlaGlnMetLysGluValGluAlaValValValAlaAlaLeuSe :::::::::::::::::::::::::::::::::::	137 174689	DP Ad
137 174690	7 eAlaMetGlnThrSerIleGluGluAlaSerLysSerMetGluSerThrLeuGluSerLe	11 17474	DP OA
117 174744	1 yValSerGlyAlaAlaAlaThrThrAlaSerAsnThrAlaThrLysI1	10 17480	Db Qy
174804	3 ANTAGCAGCAGTAACAACAGCAACAAGCAGCAACAATAAGAGCAGCAGCAGCAACAAC	17486	망

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sipA gene; sipB gene; sipC gene; sipD gene; spaT gene.
salmonella typhi.
salmonella typhi
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STSIPGNS 5393 bp
S.typhi spaT, sipB, sipC, sipD and
X82670
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Submitted (15-NOV-1994) M. Popoff, Institut Pasteur, Unite
Enterobacteries, 28 rue du Docteur Roux, 75724 Paris Cedex
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1 (bases 1 to 5393)
Hermant D., Menard,R., Arricau,N., Parsot,C. and Popoff,M.Y.
Hermant D., Menard,R., arricau,N., Parsot,C. and Popoff,M.Y.
Functional conservation of the Salmonella and Shigella effectors of entry into epithelial cells
Mol. Microbiol. 17 (4), 781-789 (1995)
96111497
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Popoff, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chemistry: Dye-primer ET; 100% of reads Chemistry: Dye-terminator Big Dye; 0% of read Assembly program: Phrap; version 0.990319 Consensus quality: 175235 bases at least Q40 Consensus quality: 176522 bases at least Q30 Consensus quality: 177171 bases at least Q20 Consensus quality: 177171 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo
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                                                                                                                                                                                                                                                                                                                                                                                                   Quality coverage: 4.48 in Q20 bases; agarose-fp Quality coverage: 4.99 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (28-FEB-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 179553) Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 179553)
Waterston, R.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Insert size: 198000; agarose-fp
Insert size: 178453; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequencing vector: M13; 100%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center project name: H_NH0758C19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens chromosome 6 clone RP11-758C19, WORKING DRAFT SEQUENCE, 12 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequencing vector: plasmid; 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence of Homo sapiens clone
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                                                                                                                                                                                                                                                                                   arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                    as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63108, USA Sep 1, 2000 this sequence version replaced gi:8568958
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                             174923 AGTAATAGTAGCAGCAACAGCAATAGCAACAGTAGCAGCATCAGCAACAACAAGAGCAAC
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                                                                                                                                                                                                                                                                                                   2 ThrAsnMetSerIleSerSerSerSerGlyProAspAsnGlnLysAsnIleMetSerGln
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AlaMetGlnThrSerIleGluGluAlaSerLysSerMetGlu---
                                                                                                                           ValLeuThrSerThrProGlnGlyValProGlnGlnAspLysLeuSerGlyAsnGluThr
                                                                                                                                                                          LysGlnIleGlnGlnThrArgGlnGlyLys---AsnThrGluMetGluSerAspAlaThr
                                                                                                                                                                                                                          MetSerIleSerSerSerGlyProAsp-----AsnGlnLysAsnIleMetSerGln
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2717 2597 2477 2417 2357 2237 2177 2060 2003 1763 1943 1643 468 428 408 388 328 296 256 236 196 157 GlnLysGluValGlyLysLeuGlnAlaAlaAlaAspMetIleSerMetPheThrGlnPhe AlaAlaGlyGlyAlaAlaGlyAlaAlaAla-----ValAsnThrValMetIleAlaValSerValAlaIleThrValIleSerIleValAlaAla TyrGlnGluMetLysAlaAlaGluGlnLysSerLysAspLeuGluGlyThrMetAspThr ACGACGCCTCGCCAAGATGTTATGGAAATCAGCTTAGCTTTAGCGAAGGCAATTACAGCC CAAAAAGAGGTCGGAGCTCTTACAGCCCAATCTGAAATGATGAAGGCGTTCACCTTGTTC AACACTCTGGGAAGTAAATGGGTAACATTAGGAGTTGGAGCACTGACAGCAGTTCCCCAA ATTTTCAACACAGGGAAAAATGCCGTTAGTAAATCCTTCCCTAACCTATCCAAAGTGATG CAAGCGATTAAACAGGCTATAAAAGCTGCTGTTAAAACTCTTACCAAAAATATTGGTAAA AlaPheIleLysThrLeuValLysAlaIleAlaLysAlaIleSerLysGlyIleSerLys CAAGGGGTCAAGCAGGCTATTGTCCAAGCGATTAAAGCAAGGACTTAAAAAAAGGGATCATG ThrValAlaThrGlnIleThrValGlnAlaValValGlnAlaValLysGlnAlaValIle GCAGCGGGAGCCAGCAGGGGGCTACAGCAGCAGCAACGACAACTTCTGTGGCAACA CTATTCACTTGCGGTCTTGGTTTAATCGGAACAGCAGCAGCAGGAGCTACA - - - GCAGCA GTTAACAAAGTGATTGGAGTGACTGTCGCTATCACTGTAGTTTCTGTTGTAGCAGCA TTCCAAAAATTGCAAGAGATCCAGAAAAAAGCTGGCAAC---AACTCCACGATGGATACC AATATGAACAAAATGTCTCTGGAATCTCAAGGACTCAAAATCGACAAAGAACGAGAAGAG CTTGGAGAGTCTACGCAAGCAGCTTTGGAAAATTTCCAAAGCACGCAAACTCAAGCCTCC CTCTCCTCCGTAGATGCGTCCCAACTACAAGAAATTCAGAACATTGTTGCTTCTGCAACG GCTTCTCAAAAAACGTGTAGAAGATACCAACAAATCTTTAGAACTATCCTCTTTAAGTTCC TGGCAACAAGCAAGTAAGATTGCTGCAAAACCAAACCGAAAGCCCTAGCGAAACACAACAG LeuGlyLysGlyIleMetGlnMetGlnLeuSerGluMetGlnGlnAsnValAlaGlnPhe ThrAlaValArgGlnAlaIleThrAlaAlaIleLysAlaAlaValLysSerGlyIleLys LeuGlyGluAlaThrLysSerAlaLeuSerAsnTyrAlaSerThrGlnAlaGlnAlaAsp ValThrProArgSerGluValIleGluIleGlyLeuAlaLeuAlaLysAlaIleGlnThr LeuGlnSerLeuSerAlaAlaGlnMetLysGluValGluAlaValValValAlaAlaLeu ---AlaThr 1942 467 2656 447 2596 427 2536 215 1882 2776 487 2716 407 2476 2416 2356 2236 307 2176 2002 195 1762 387 367 2296 2119 2059 235 347 327 295 275 255

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gene	gene CDS	gene CDS	JOURNAL COMMENT FEATURES SOURCE gene CDS	TITLE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS
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WQLGMPELLLIVATCLSSYGWFILKKLERQCESKSITAINAYAMVIAGILSLAHSAIT
EVWNPLPVENPYLFLQSIGALVIFSNLICYNLFAKLLRSFSSTFLSFCNLVMPLFASF
EGWLLLGESFPPGLLFAVGFMVLGCRLIYHEEFRQGYVLSSE"
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complement(4206..5162)
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2822. .4132
/gene="TC0868"
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Glimmer2; putative"
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7785. .8552
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/gene="TC0870"
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PID:1565235 GB:AL009126; identified by sequence
similarity; putative"
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/gene="TC0869"
/note="conserved hypothetical protein; identified
Glimmer2; putative"
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                                                                                                        /product="ParA family
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    ThrLeuGlyGluAlaThrLysSerAlaLeuSerAsnTyrAlaSerThrGlnAlaGlnAla
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EVEISAYTQGEFLDLCRGPHLPSTAPVKAFKLLRTSSAYWKGDPSRESLIRIYGVSFP
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ACCESSION

Chlamydia muridarum, AE002353 AE002160 AE002353.2 GI:81633

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98 dd of DNA 85 of the

linear complete

BCT 26-MAY-2000 genome.

VERSION KEYWORDS

SOURCE ORGANISM

Chlamydia Chlamydia

muridarum GI:8163337

REFERENCE

AUTHORS

Chlamydia muridarum
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.

1 (bases 1 to 9983)
Read, T.D., Brunham, R., Shen, C., Gill, S.R., Heidelberg, J.
White, O., Hickey, E.K., Peterson, J., Umayam, L.A., Utterba

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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 10653)
Stephens,R.S., Kalman,S., Lammel,C.J., Fan,J., Marathe,R., Aravind,L., Mitchell,W.P., Olinger,L., Tatusov,R.L., Zhao,Q., Koonin,E.V. and Davis,R.W.
Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (20-MAY-1998) Program in Infectious Diseases, University of California, 235 Warren Hall, Berkeley, CA 94720-7360, USA
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SCFQKSPQMDRLAIRRLLENSVISSEGIGWTWISECRQELYVAKKQGFIERVALVLGE
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SLEETVLKVPTEKIPIENEGISVPSIRPAIVSAPLSCPTFSQQPYLKTEMATIVSRDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KELVRMLHVFWANLGIEKVSFPPIIAFGENAAFPHAIPTNRSLKKGDVVLIDIGVCYE
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VALAQEGALHVGESFEQLVENTVQKLVFSRNARAFDYAWLDILWKLGKPEKAFDGEMI
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                                                                                                                                                          RRLVLDDDFM"
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Tatusov,R.L., Zhao,Q.,
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/gene="(
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HITACHI CHEM CO LTD

None
OC Artificial sequences.
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PN JP 1
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Izutsu,H., Obara,K. and Matsumoto,A.
IZUTSU,H., Obara,K. and Matsumoto,A.
THEREFOR AS WELL AS DIAGNOSTIC MEDICINE FOR CHLAMYDIA PNEUMONIA
THEREFOR AS WELL AS DIAGNOSTIC MEDICINE FOR CHLAMYDIA PNEUMONIA
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JP 1997015243-A/2.
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16/12,C07K19/00,
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                                                                                                /organism="unidentified"
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AE001328.1 GI:3329015
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Chlamydiaceae; Chlamydia

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1 (bases 1 to 1296)
1 Izutsu, H., Obara, K. and Matsumoto, A.
1 Izutsu, H., Obara, K. and Matsumoto, Antifer Properties and Production of ANTI-CHLAMYDIA PNEUMONEAE ANTIBODY Patent: JP 1997009976-A 2 14-JAN-1997;
                                                                                                                     DNA encoding a fusion Chlamydia pneumoniae. E12526
                                                                               unidentified.
unidentified
                                                                     unclassified.
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JP 1997009976-A/2.
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Alignment Pred. No.:
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Best Local Similarity:
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OS None
OC Note:
OC Artificial sequences.
PN JP 197009976-A/2
PN JP 197009976-A/2
PN JP 197009976-A/2
PP 14-MAR-1996 JP 1996057409
PR 28-APR-1995 JP 95P 106006
PI IZUTSU HIROSHI, OBARA KAZUHIKO, MATSUMOTO AKIRA PC
C12N15/09,C12R1:01),
PC G01N33/569,G01N33/571/A61K39/395,A61K49/00,C12P21/08, PC
(C12N15/09,C12R1:01),
PC G01N3/569,G01N33/571/A61K39/395,A61K49/00,C12P21/08, PC
(C12N15/09,C12R1:19),(C12P21/02,C12R1:19),(C12P21/02,C12R1:9)
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PC (C12N1/21,C12R1:19),(C12P21/02,C12R1:19)
PC (C12R1:91);
CC topology: Linear;
FH Key Linear;
FH Key Jorganism='Artificial sequences' FT
mat_peptide 1. 1296
FT misc_feature 1. 1296
FT misc_feature 1. 484. 1296
FT misc_feature 484. 1296
FT misc_feature 484. 1296
FT misc_feature 484. 1296
FT mote='antigen peptide coding region'.
GlyAlaAlaAlaThrThrAlaSerAsnThrAlaThrLysIleAlaMetGlnThrSerIle
                                                                                                                                                                                                                                                                                                                      ValAlaAlaGlyLysGluSerSerGluSerGlnLysAlaGlyAlaAspThrGlyValSer
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                                                                                                                                                                                                                                                                                        GTTGCTGCTGGGAAAGAATCCTCAGAAAGTCAAAAAGGCAGGTGCTGATACTGGAGTATCA
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299 c 325 g
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Alignment :
Pred. No.:
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                                                         US-09-889-314-2 (1-496) x E12542
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Best Local Similarity:
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         24
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                                                                                                                          Scores
                                                                                                                                                                                         INFECTION
Patent: JP 1997015244
HITACHI CHEM CO LTD
OS Chlamydia pneumc
PN JP 1997015244-A
PD 17-JAN-1997
PF 14-MAR-1996 JP 1
PR 28-APR-1995 JP 9
PI 1ZUTSU HIROSHI,
PC G01N33/569//A6IH
PC G01N33/569//A6IH
PC G01N33/569//A6IH
PC Key
FH Key
FH Key
FH SOURCE
FT SOURCE
FT mat_peptide
FT mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                             DNA end
E12542
                                                                                                                                                                                                                                                                                                                                                  Izutsu,H. and Matsumoto,A.

MEASURING METHOD FOR ANTICHLAMYDIA-PNEUMONIA ANTIBODY
THEREFOR AS WELL AS DIAGNOSTIC MEDICINE FOR CHLAMYDIA
                                                                                                                                                                                                                                                                                                                                                                                                           E12542.1 GI:32513
JP 1997015244-A/2.
                                                                                                                                                                                                                                                                                                                                                                                             unidentified
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28-APR-1995 JP 95P 106011
1ZUTSU HIROSHI, MATSUMOTO AKIRA
G01N33/571,CO7K14/295,CO7K16/12,G01N33/53,
G01N33/569//A61K49/00,C12N15/09;
strandedness: Double;
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JP 1997015244-A/2
                                                                                                                                                                                                                                            topology: Linear;
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                                                                                                                                                  /organism="unidentified"
/db_xref="taxon:32644"
181 c 187 g 15
                                                                                                                                                                                  /product='
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                                                                          1.63e-59
1245.00
100.00%
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                                                         (1-813)
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1 .813
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peptide
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                                                                                Length:
Matches:
Conservative:
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AUTHORS
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       Query Match:
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                                                                                                                                                 Unknown.
Unknown.
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Дb
                         Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                             Sequence
AR122115
AR122115.
                                                                                                                                                            I (bases 1 to 1296)
Izutsu,H., Obara,K. and Matsumoto,A.
DNA encoding Chlamydia pneumoniae an
Patent: US 6165478-A 18 26-DEC-2000;
                                                                                                                                                                                                                Unclassified.
                                                                                                              a
                                                                                                                                                                                                                                                                                     18
                                                                                                                                    Location/Qualifiers
1. .1296
                                                                                                             /organism="unknown"
299 c 325 g
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1 (bases 1 to 813)
1 (bases 1 to 813)
1 routsu, H. and Matsumoto, A.
1 routsu, H. and Matsumoto, A.
ANTIGEN POLYPEPTIDE INVOLVED WITH CHLAMYDIA PNEUMONEAE, DNA CODING FOR THE SAME, RECOMBINANT VECTOR CONTAINING THE DNA, TRANSFORMANT CONTAINING THE VECTOR, AND PRODUCTION OF ANTI-CHLAMYDIA PNEUMONEAE Patent: JP 1997009974-A 2 14-JAN-1997;
                                                                            DNA encoding an antigen
E12521
E12521.1 GI:3251354
JP 1997009974-A/2.
                                                              unidentified
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OS Chlamydia pneumoniae

PN JP 1997009974-A/2

PD 14-JAN-1997

PF 20-SEP-1995 JP 1995242095

PR 20-SEP-1994 JP 94P 224711, 28-APR-1995 JP

IZUTSU HIROSHI, MATSUMOTO AKIRA

PC C12N15/09,C07H21/04,C07K14/295,C07K16/12,C12

PC C12P21/08,

PC C12N15/09,C07H21/04,C07K14/295,C07K16/12,C12

PC C12P21/08,

PC C12P21/08,C12PX1:91);

PC (C12P21/08,C12PX1:91);

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PC (C12P21/08,C12PX1:91);

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C12P21/08,
G1N33/53,G0N33/571//A61K39/118,A61K39/118,A61K39/118, PC
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/db_xref="taxon:32644"
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PATENT: JP 19
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OS Chlamydi
PA JP 19970
PD J7-JAN-1
PF 14-MAR-1
PF 28-APR-1
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PC G01N33/5
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1 (bases 1 to 777)

Izutsu,H. and Matsumoto,A.

MEASURING METHOD FOR ANTICHLAMYDIA-PNEUMONIA ANTIBODY AND REAGEN
MEASURING METHOD FOR CHLAMYDIA PNEUMONIA
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28-APR-1995 JP 95P 106011
IZUTSU HIROSHI, MATSUMOTO AKIRA
G01N33/571,C07K14/295,C07K16/12,G01N33/53,
G01N33/569//A6IK49/00,C12N15/09;
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Jp 1997015244-A/3
17-JAN-1997
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/db_xref="taxon:32644"
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Percent Similarity:
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Similarity:
                                                                                                                                         Unknown.
Unknown.
                                                                                                                                                                          AR122106
Sequence
AR122106
                                                                             1 (bases 1 to 813)
Izutsu,H., Obara,K. and Matsumoto,A.
DNA encoding Chlamydia pneumoniae an
Patent: US 6165478-A 4 26-DEC-2000;
Location/Qualifiers
1 813
                                                                                                                                Unclassified.
                                                                                                                                                                   AR122106
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                                                           /organism="unknown"
181 c 187 g
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s 6165478.
Matches:
Conservative:
Mismatches:
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                                                                                     DNA encoding
E12522
E12522.1 GI:
JP 1997009974
1 (bases 1 to 777)

Izutsu, H. and Matsumoto, A.

ANTIGEN POLYPEPTIDE INVOLVED WITH CHLAMYDIA PNEUMONEAE, DNA CODING FOR THE SAME, RECOMBINANT VECTOR CONTAINING THE DNA, TRANSFORMANT CONTAINING THE VECTOR, AND PRODUCTION OF ANTI-CHLAMYDIA PNEUMONEAE
                                                                  unidentified. unidentified
                                                        unclassified.
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1997009974-A/3.
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HITACHI CHEM CO LTD

OS Chlamydia pneumoniae
PN Jp 1997009974-A/3

PD 14-JAN-1997

PP 20-SEP-1995 JP 1995242095
PR 20-SEP-1995 JP 1995242095
PR 20-SEP-1994 JP 94P 224711, 28-APR-1995 JP 95P 106010 PI
IZUTSU HIROSHI, MATSUMOTO AKIRA
PC C12N15/09, C07H21/04, C07K14/295, C07K16/12, C12N1/21, C12N15/02,
PC C12P21/08, C07H21/04, C07K14/295, C07K16/12, C12N1/21, C12N15/02,
PC G01N33/53, G01N33/571//A61K39/118, A61K39/118, A61K39/118, PC
(C12N1/21, C12R1:91);
CC strandedness: Double;
CC topology: Linear;
FH Key Location/Qualifiers
FH Source 1. .777
FT source 1. .777

FT source 1. .777

FT source 1. .777
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              AlaLysLeuGluThrProGluLeuProLysProGlyValThrProArgSerGluValIle
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/db_xref="taxon:32644"
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HITACHI CHEM CO LTD

OS Chlamydia pneumoniae
PN JP 1995304404-A/2
PD 22-NOV-1996
PF 28-APR-1995 JP 1995106014
PI 12UTSU HIROSHI, MATSUMOTO AKIRA
PC G01N33/59 C07K14/295,G01N33/53,G01N33/571//A61K49/00, PC
C12N15/09,C12P21/02,
PC (C12P21/02,C12R1:19);
CC strandedness: Double;
CC topology: Linear;
CC topology: Linear;
CC fragment_type: N-Terminal Fragment;
FH Key /organism='Chlamydia pneumoniae' FT
FT Source /organism='Chlamydia pneumoniae' FT
IleAla
                                     GATACAAACATGTCTATTTCATCTTCTTCAGGACCTGACAATCAAAAAATATCATGTCT
                                              AspThrAsnMetSerIleSerSerSerSerGlyProAspAsnGlnLysAsnIleMetSer
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Izutsu, H. and Matsumoto, A.
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                                                                                                                                                                          /organism="unidentified"
/db_xref="taxon:32644"
241 c 231 g 21
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Location/Qualifiers
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pneumoniae'
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Percent Similarity:
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AR122107
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Izutsu,H., Obara,K. and Matsumoto,A.
Izutsu,Gandg Chlamydia pneumoniae antigenic polypeptide
Patent: US 6165478-A 7 26-DEC-2000;
                                                                                                           Unknown
                                                                                                                  Unknown.
                                                                                                    Unclassified
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Length:
Matches:
Conservative:
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Patent: JP 1996143594-A 2
HITACHI CHEM CO LTD
OS Chlamydia neumonie
DP 1996143594-A/2
PD 04-JUN-1996
PF 28-APR-1995 JP 199519
PR 20-SEP-1994 JP 94P
PI IZUTSU HIROSHI, MATS
PC C07K14/295,C07K16/12
PC C12R1:91),C(12N1/21,
PC C1ZR1:91),C(12N1/21,
PC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
FH Key
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E11479.1 GI:22025115
JP 1996143594-A/2.
unidentified.
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                                                                                                                                                                  IZUTSI, H. AND MATSUMOTO, A.
ANTIGEN LEYPEPTIDE FOR CHLAMYDIA NEUMONEAE,
SAME, RECOMBINANT VECTOR CONTAINING THE DNA,
CONTAINING THE RECOMBINANT VECTOR, AND PRODUC
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20-SEP-1994 JP 94P 224711
20-STEP-1994 JP 94P 224711
20-STEP-1994 JP 94P 224711
COTK14/295, COTK16/12, C12N15/02, C12N15/09, C12P21/08//C12N1/21, C12P21/08,
C12P21/08,
C12R1:91), (C12N1/21, C12R1:19);
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		TOGGUCTGTCGCTTGCGGTATTCGGAATCTTGCACGCCCTCGCTCAAGCCTTCGTCAC
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	Db 1921	CAGGCCATTATCGCCGGCATGGCGGCCGACGCGCTGGGCTACGTCTTGCTGGCGTTCGCG 1980
	Qy 391	ThrSerLysTrpValThrValGlyValGlyValValValAlaAlaProAlaLeuGlyLys 410
	Db 1981	ACGCGAGGCTGGATTGCCCCCATTATGATTCTTCTCGCTTCCGGCGGCATCGGGATG 2040
	Qy 411	GlyIleMetGlnMetGlnLeuSerGluMetGlnGlnAsnValAlaGlnPheGlnLysGlu 430
	Db 2041	CCCGCGTTGCAGGCCATGCTGTCCAGGCAGGTAGATGACGACCATCAGGGACAGCTTCAA 2100
	QY 431	ValGlyLysLeuGlnAlaAlaAlaAspMetIleSerMet 443
	Db 2101	CGCGGCTCTTACCAGCCTAACT
	RESULT 25 AR122109 LOCUS	
	ACCESSION VERSION KEYWORDS	AR122109 AR122109.1 GI:14106426
	SOURCE ORGANISM	
	REFERENCE	UnclassIlled. 1 (bases 1 to 1048) 1 vitsu.H., Obara,K. and Matsumoto,A.
	TITLE JOURNAL FEATURES SOURCE	DNA encoding Chlamyd Patent: US 6165478-A Location/Qu e 1. 1048
	BASE COUNT ORIGIN	360 a 241 c 231 g 216 t
	Alignment Sc Pred. No.: Score: Percent Simi Best Local S Query Match: DB:	. No.: 2.67e-60 Length: 1048 e: 1262.00 Matches: 262 ent Similarity: 100.00% Conservative: 0 Local Similarity: 100.00% Mismatches: 0 y Match: 53.27% Indels: 0 Gaps: 0
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		spThrAsnMetSerIleSerSerSerSerGlyProAspAsnGlnLysAsnIleMetSer 20
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ACGCGAGGCTGGATGGCCTTCCCCCATTATGATTCTTCTCCGCCTTCCGGCCGCATCGGGATG 2040
                              ThrSerLysTrpValThrValGlyValGlyValValValAlaAlaProAlaLeuGlyLys 410
                                                                 CAGGCCATTATCGCCGGCATGGCGGCCGACGCGCTGGGCTACGTCTTGCTGGCGTTCGCG
                                                                                                                                                                                                                                                                         GTGCCGGCAGCGCTCTGGGTCATTTTCGGCGAGGACCGCTTTCGCTGGAGCGCGACGATG 1830
                                                                                                                                                                                                                                                                                                                                           ACTGTCTTTATCATGCAACTCGTAGGACAG---
                                                                                                                                                                                                                                                                                                                                                                         ThrValGlnAlaValValGlnAlaValLysGlnAlaValIleThrAlaValArgGlnAla
                                                                                                                                                                                                                                                                                                                                                                                                              TTCAACCCAGTCAGCTCCTTCCGGTGGGCGCGGGGCATGACTATCGTCGCCGCACTTATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGCTGCTTCCTAATGCAGGAGTCGCATAAGGGAGAGCGTCGACCGATGCCCTTGAGAGCC
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                                                                                                 SerLysValIleSerSerLeu-----
                                                                                                                                                                  GlyIleSerLysValPheAlaLysGlyThrGlnMetIleAlaLysAsnPheProLysLeu 383
                                                                                                                                                                                                        ATCGGCCTGTCGCTTGCGGTATTCGGAATCTTGCACGCCCTCGCTCAAGCCTTCGTCACT
                                                                                                                                                                                                                                      SerGlyIleLysAlaPheIleLysThrLeuValLysAlaIleAlaLysAlaIleSerLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --AlaAlaAla----
                                                                                                                                      ----ACCAAACGTTTCGGCGAGAAG
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CC G01N33/531,G01N33/571/A61K49/00,C07K14/245,C07K14/39, PC

C07K16/12,C07K19/00,

PC (C12N1/21,C12R1:19),(C12N15/09,C12R1:01),(C12P21/02,C12R1:19);

CC strandedness: Double;

CC topology: Circular;

EH Key Location/Qualifiers

EH Key 1 .5438

FT source /organism='Artificial sequences'.
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HITACHI CHEM CO LTD
OS None
OC Artificial sequences.
PN JP 1997015243-A/3
PD 17-JAN-1997
PD 17-JAN-1997
PF 15-MAR-1996 JP 1996058609
PF 28-APR-1995 JP 95P 106009
PR 28-APR-1995 JP 95P 106009
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IZULSU,H., Obara,K. and Matsumoto,A.

MEASURING METHOD FOR ANTI-CHLAMYDIA PNEUMONIA ANTIBODY
THEREFOR AS WELL AS DIAGNOSTIC MEDICINE FOR CHLAMYDIA I
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JP 1997015243-A/3.
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Mismatches:
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PN p 1997009976-A/3

PD 14-JAN-1997

PF 14-MAR-1996 JP 1996057409

PR 28-APR-1995 JP 95P 106006

PI IZUTSU HIROSHI, OBARA KAZUHIKO, MATSUMOTO AKIRA PC

C12N15/09,C07H21/04,C07K14/295,C07K14/47,C07K19/00,C12N1/21, PC

C12P21/02,

PC G01N33/569,G01N33/571//A61K39/395,A61K49/00,C12P21/08, PC

(C12N1/21)C12R1:19),(C12P21/02,C12R1:19),(C12P21/02,C12R1:

PC (C12N1/21)C12R1:19),(C12P21/02,C12R1:19),(C12P21/02,C12R1:

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                                                                                                        CAGCTTCAA---GGATCGCTCGCGGCTCTTACCAGCCTAACTTCGATC
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                                                                                              GlnMetLysGluValGluAlaValValValAlaAlaLeuSerGlyLysSerSerGlySer
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                                                    ATACAGCAAACACGTCAGGGTAAAAACACTGAGATGGAAAGCGATGCCACTATTGCTGGT
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             CAGAAGTCTAAAGATCTCGAAGGAACAATGGATACTGTCAATACTGTGATGATCGCGAA-
                       GlnLysSerLysAspLeuGluGlyThrMetAspThrValAsnThrValMetIleAlaVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unclassified.
1 (bases 1 to 5438)
Izutsu,H., Obara,K. and Matsumoto,A.
Izutsu,H., Obara,K. and matsumoto,A.
DNA encoding Chlamydia pneumoniae antigenic patent: US 6165478-A 25 26-DEC-2000;
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HITACHI CHEM CO 1
OS NONe
OC Artificial:
PN JP 199701524
PD 17-JAN-1997
PF 14-MAR-1996
PR 28-APR-1995
PI IZUTSU HIROS
                                                                                                                                                                                                Nucleotide :
pneumoniae a
E12544
E12544.1 GJ
                                                                                                                     1 (bases 1 to 5658)
Izutsu,H. and Matsumoto,A.
MEASURING METHOD FOR ANTICHLAMYDIA-PNEUMONIA ANTIBODY AND REAGENT
                                                                                                 THEREFOR AS WELL AS DIAGNOSTIC INFECTION
                                                                                                                                                      unclassified
                                                                                                                                                                   unidentified
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                                                                                                                                                                                        1997015244-A/4.
                             Artificial sequences.
JP 1997015244-A/4
17-JAN-1997
           14-MAR-1996 JP 1996057410
28-APR-1995 JP 95P 1060:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -GTGCCGGCAGCGCTCTGGGTCATTTTCGGCGAGGACCGCTTTCGCTGGAGC
                                                                                      JP 1997015244-A
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                                                                                                                                                                                                                 sequence of pCPN533 a antigen gene.
 HIROSHI,
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  MATSUMOTO AKIRA
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                                                               LysSerAlaLeuSerAsnTyrAlaSerThrGlnAlaGlnAlaAspGlnThrAsnLysLeu
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strandedness: Double;
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                                                                                                 PALE PATENTS IN TACTOR, AND ENDUCTION OF ANTI-CHIAMIDIA PREDMOREAE.

PATENT: JP 1997009974-A 4 14-JAN-1997;

HITACHI CHEM CO LTD

OS None

OC Artificial sequences.

PN JP 1997009974-A/4

PD 14-JAN-1997

PF 20-SEP-1995 JP 1995242095

PF 20-SEP-1995 JP 224711, 28-APR-1995 JP 95P 106010 PI

IZUTSU HIROSHI, MATSUMOTO AKIRA

PC C12N15/09,C07H21/04,C07K14/295,C07K16/12,C12N1/21,C12N15/02,

PC C12P21/08,

PC G01N33/53,G01N33/571//A61K39/118,A61K39/118,A61K39/118, PC

(C12N1/21,C12R1:91),

PC (C12P21/08,C12R1:91);

CC strandedness: Double;

CC topology: Circular;

FH Key Location/Qualifiers

FH Source /organism-'Artificial sequences'.
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                                                                                                                                                                                                                                                                                                                                                   IZUTSU, H. and Matsumoto, A.
ANTIGEN POLYPEPFIDE INVOLVED WITH CHLAMYDIA PNEUMONEAE, DNA CODING
FOR THE SAME, RECOMBINANT VECTOR CONTAINING THE DNA, TRANSFORMANT
CONTAINING THE VECTOR, AND PRODUCTION OF ANTI-CHLAMYDIA PNEUMONEAE
PATENT: JP 1997009974-A 4 14-JAN-1997;
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Nucleotide sequence of pCPN533 c
pneumoniae antigen gene.
E12523
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                                     /organism="unidentified"
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              GCGGTTGCTGGCGCCTA-TATCGCCGACATCACCGATGGGGAAGATCGGGCTCGCCACTT
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                                                                                       IleValAlaAlaIlePheThrCysGlyAlaGlyLeuAlaGlyLeu----AlaAlaGly
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TITLE
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No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      ThrLysGlnIleGlnGlnThrArgGlnGlyLysAsnThrGluMetGluSerAspAlaThr 60
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                                                                                                                                                                                                                                                                               Sequence
AR122110
                                                                                                                                                                                                    Unclassified.

1 (bases 1 to 5658)

Izutsu, H., Obara, K. and Matsumoto, A.

DNA encoding Chlamydia pneumoniae antigenic
Patent: US 6165478-A 10 26-DEC-2000;
                                                                                                                                                                                                                                                        Unknown
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                                                                                                                                                                        /organism="unknown"
1477 c 1428 g
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1282.00
62.59%
56.65%
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US 6165478.
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Matches:
Conservative:
Mismatches:
Indels:
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1990	TGACTGTCTTCTTATCATGCAACTCGTAGGACA	Db
	11 ThrGlnIleThrValGlnAlaValValGlnAlaValL ::::	Qy
1948	ATCGTCGCC	Db
310	rThrValAla	Qy
1888	TGCTTCCTAATGCAGGAGTCGCATAAGGGAGAGCGTCGACCGATGCCC	Db
306		Qy
1828	ATCTCCTTGCATGCACCATTCCTTGCGGCGCGCGCTGCTCAACGGCCTCAAC	Db
306	GlyAlaAlaAlaAla	Qy
1768	ATGAGCGCTTGTTTCGGCGTGGGTATGGTGGCAGGCCCGTGGCCGGGGGACTG	Db
300	AlaGlyGlyAla	Qy
1708	50 GCGGTTGCTGGCGCCTA-TATCGCCGACATCACCGATGGGGAAGATCGGGGCTCGCCACTT	Db
295	0 AlaAlaValGlyAlaAla	Qy
1649	90 ATCTAATCGATGATCCTCTACGCCGGACGCATCGTGGCCGGCATCACCGGCGCCACAGGT	Db
289	72 IleValAlaAlaIlePheThrCysGlyAlaGlyLeuAlaGlyLeuAlaAlaGly	Qy
1589	111111 ::: 31 ATCGCGAA-GGGGTTCGAATTGCCATGGGGGCCCTTAATTAATTAACTCGAGAGATCCAG	Db
271	61 IleAlaValSerValAlaIleThrValIleSer	Qy
1530	71 GCTGCCGAACAGAAGTCTAAAGATCTCGAAGGAACAATGGATACTGTCAATACTGTGATG	Db
260	1 AlaAlaGluGlnLysSerLysAspLeuGluGlyThrMetAspThrValAsnThrValMet	Qy
1470	11 GGTCTAGAAAAGCAAGCGATAAAAATCGATAAAGAACGAGAAGAATACCAAGAGATGAAG	Дb
240	21 GlyLeuGluLysGlnAlaIleLysIleAspLysGluArgGluGluTyrGlnGluMetLys	Qy
4-	Link	р <sub>р</sub> Х
3	201   Traccora   51 011C0   Tours   Traccord   Traccord	
1350	181 GluVallIeGluIieGlyLeuAlaLeuAlaLysAlaILeGlnTnrLeuGlyGLuAlaTnr 	P &
i io	31 TCGGGTTCCGCAAAATTGGAAACACCTGAGCTCCCCAAGCCCGGGGTGACACCAAGATCA	рь
180	1 SerGlySerAlaLysLeuGluThrProGluLeuProLysProGlyValThrProArgSer	Qy
1230	1171 AGTGCCGCGCAAATGAAAGAAGTCGAAGCGGTTGTTGTTGTTGCCCTCTCAGGGAAAAGT	Db
160	41 SerAlaAlaGlnMetLysGluValGluAlaValValValAlaAlaLeuSerGlyLysSer	Qy
1170	1111 ACCTCTATTGAAGAGGCGAAGCAAAAGTATGGAGTCTACCTTAGAGTCACTTCAAAGCCTC	DЪ
140	hrSerIleGluGluAlaSerLysSerMetGluSerThrLeuGluSerLeuGluSerLeu	Qy
1110	TTGCTATGCAG	Db
120	lyValSerGlyAlaAlaAlaThrThrAlaSerAsnThrAlaThrLysIleAlaMetGln	Qy
1050		Db
100	lnGlnGlyValAlaAlaGlyLysGluSerSerGluSerGlnLysAlaGlyAlaAspThr	Qy
990	CTGGTGCTTCTGGAAAAGACAAAACTTCCTCGACTACAAAAACAGAAAACAGCTCCA	Ф
80	AlaGlyAlaSerGlyLysAspLysThrSerSerThrThrLysThrGluThrAlaPro	Qy

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LOCUS
   Percent Similarity:
                                     Pred. No.:
                                                     Alignment
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PATENCIST P1997015243-A 1 17-JAN-1997;
HTTACHI CHEM CO LTD

None
OC Artificial sequences.
PN JP1997015243-A/1
PD 17-JAN-1995
PF 15-MAR-1996 JP 1996058609
PF 17-JAN-1997
PF 17-JAN-1996 JP 1996058609
PF 17-JAN-1997
PF 1997015243-A/1
PF 1997015243
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IZULTSU,H., OBATA,K. and Matsumoto,A.
IZULTSU,H., OBATA,K. and MATSUMOTO,A.
MEASGRING METHOD FOR ANTI-CHLAMYDIA PNEUMONIA ANTIBODY AND REAGINEEPOR AS WELL AS DIAGNOSTIC MEDICINE FOR CHLAMYDIA PNEUMONIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFECTION
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449 c 486 g
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AlaLysLeuGluThrProGluLeuProLysProGlyValThrProArgSerGluValIle
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                                                                                                                                     TCTGTTGCCATTACAGTTATTTCTATTGTTGCTGCTATTTTTACATGCGGAGCTGGACTC
                                                                                                                                                                                                                         SerValAlaIleThrValIleSerIleValAlaAlaIlePheThrCysGlyAlaGlyLeu
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Indels:
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ANTI-CHLAWYDIA PNEUMONEAE ANTIBODY;

PATENT: UP 1997009976-A 1 14-JAN-1997;

OS ARTIFICIAL SEQUENCES.

PN JP 1997009976-A/1

PD 14-JAN-1997

PP 120TSU HIROSHI, OBARA KAZUHIKO, MATSUMOTO AKIRA PC C12R15/09,C07811/04,C07K14/295,C07K14/47,C07K19/00,C12R1/21, PC C12R15/09,C12R1:01), (C12P21/02,C12R1:19), (C12P21/02,C12R1:19), PC (C12N15/09,C12R1:01), (C12P21/02,C12R1:19), (C12P21/02,C12R1:19), PC (C12N15/09,C12R1:19), (C12P21/02,C12R1:19), PC (C12N15/09,C12R1:19), (C12P21/02,C12R1:19), PC (C12R1:19);

PC (C12N15/09,C12R1:19), (C12P21/02,C12R1:19), (C12P21/02,C12R1:91), PC (C12R1:19), (C12P21/02,C12R1:19), (C12P21/02
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           ThrSerThrProGlnGlyValProGlnGlnAspLysLeuSerGlyAsnGluThrLysGln 43
                                                                                    DNA encodi
Chlamydia
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DIHYDROFOLIC ACID REDUCTASSE-CHLAMYDIA PNEUMONEAE ANTIGEN FUSED
PROTEIN, DNA CODING FOR THE SAME, RECOMBINANT VECTOR CONTAINING
DNA, TRANSFORMANT CONTAINING THE VECTOR, AND PRODUCTION OF
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                          TCGAAAGTCATCTCGTCTTTACCAGTAAATGGGTCACGGTTGGGGGTTGGGGTTGTAGTT
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Izutsu,H., Obara,K. and Matsumoto,A.
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DNA encoding Chlamydia pneumoniae and
Patent: US 6165478-A 17 26-DEC-2000;
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LysGlnAlaIleLysIleAspLysGluArgGluGluTyrGlnGluMetLysAlaAlaGlu GluIleGlyLeuAlaLeuAlaLysAlaIleGlnThrLeuGlyGluAlaThrLysSerAla GlnMetLysGluValGluAlaValValValAlaAlaLeuSerGlyLysSerSerGlySer GlnAlaValIleThrAlaValArgGlnAlaIleThrAlaAlaIleLysAlaAlaValLys AlaAlaAlaThrThrValAlaThrGlnIleThrValGlnAlaValValGlnAlaValLys GAAATCGGACTCGCGCTTGCTAAAGCAATTCAGACATTGGGAGAAGCCACAAAATCTGCC CAAATGAAAGAAGTCGAAGCGGTTGTTGTTGCTGCCCTCTCAGGGAAAAGTTCGGGTTCC GluMetThrGlnLysAlaThrLysLeuGlyAlaGlnIleLeuLysAlaTyrAlaAlaIle ValAlaGlnPheGlnLysGluValGlyLysLeuGlnAlaAlaAlaAspMetIleSerMet CAAGCTGTTATCACAGCTGTCAGACAAGCGATCACCGCGGCTATAAAAAGCGGCTGTCAAA GCTGGACTCGCTGCGGGAGCTGCTGTAGGTGCAGCGGCAGCTGGAGGTGCAGCAGGAGCT AlaGlyLeuAlaAlaGlyAlaAlaValGlyAlaAlaAlaAlaGlyGlyAlaAlaGlyAla AAGCAAGCGATAAAAATCGATAAAGAACGAGAAGAATACCAAGAGATGAAGGCTGCCGAA PheThrGlnPheTrpGlnGlnAlaSerLysIleAlaSerLysGlnThrGlyGluSerAsn GTCGCTCAATTTCAGAAAGAAGTCGGAAAACTGCAGGCTGCGGCTGATATGATTTCTATG GCTGCCGCAACCACGGTAGCAACACAAATTACAGTTCAAGCTGTTGTCCAAGCGGTGAAA 1323 1203 1143 483 1743 1623 1563 1503 1443 1383 1263 1083 1023 903 1863 463 443 423 1683 403 383 363 323 303 283 263 223 183 963 163

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44 IleGlnGlnThrArgGlnGlyLysAsnThrGluMetGluSerAspAlaThrIleAlaGly 63
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RIZUTSU, H. and Hagiwara, T.

RECOMBINANT VECTOR AND TRANSFORMANT CONTAINING THE SAME, AND RECOMBINANT VECTOR AND THE SAME, AND RECOMBINANT VECTOR AND THE SAME, AND THE SAME, AND PRODUCTION OF CHAMYDIA PROBUNCIAN AND THE SAME, AND PRODUCTION OF CHAMYDIA PROBUNCATION OF CALCANT OF CHAMYDIA PROBUNCATION OF CHAMYDIA PR
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                                                                        ThrSerThrProGlnGlyValProGlnGlnAspLysLeuSerGlyAsnGluThrLysGln 43
                                                ACATCGACACCCCAGGGCGTGCCCCAACAAGATAAGCTGTCTGGCAACGAAACGAAGCAA
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JP 1998210978-A/1.
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Chlamydia pneumoniae gene
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31-JAN-1997 JP 1997018523
IZUTSU HIROSHI, HAGIWARA TOSHIKATSU
C12N15/09,C07H21/04,C07K14/295,C12N1/21,C12N5/10,C12N7/00, PC
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/db_xref="taxon:32644"
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423	AlaAlaProAlaLeuGlyLysGlyIleMetGlnMetGlnLeuSerGluMetGlnGlnAsn 	404	Qy
1200	CGAAAGTCATCTCGTCTCTTACCAGTAAATGGGTCACGGTTGGGGTTGGGGTTGTAGT	1141	DЬ
403	SerLysValIleSerSerLeuThrSerLysTrpValThrValGlyValGlyValValValVal	384	Qy
383	GlyIleSerLysValPheAlaLysGlyThrGlnMetIleAlaLysAsnPheProLysLeu	364	Qy
1140		1081	Db
363	aPheIleLysThrLeuValLysAla	344	Оy
1080		1021	
343	alIleThrAlaValArgGlnAlaIleThrAlaAlaIleLysAlaAlaVal	324	ОУ
1020		961	
323	ValAlaThrGlnIleThrValGlnAlaValValGln	304	Qу
960		901	ДЪ
303	aAlaValGlyAlaAlaAlaAlaGlyGlyAlaAlaGlyAla 	284 841	Оу
283	allleSerIleValAlaAlaIlePheThrCysGlyAlaGlyLeu 	264 781	Оу
263 780	hrvalasnThrvalMetI             CTGTCAATACTGTGATGA	244 721	Ор
243 720	3luArgGluGluTyrGlnGluMetLys                    AACGAGAAGAATACCAAGAGATGAAC	224 661	dq Qy
223	nAlaGlnAlaAspGlnThrAsnLysLeu	204	Фр
660		601	
203	uAlaLysAlaIleGlnThrLeuGlyGluAlaThrLysSerAla 	184 541	Фр
183	uLeuProLysProGlyValThrProArgSerGluValIle	164	ДЬ
540		481	
163	lualavalvalvalAlaAlaLeuSerGlyLySSerSerGlySer	144	ОУ
480		421	
143	tGluSerThrLeuGluSerLeuGlnSerLeuSerAlaAla	124	Qу
420		361	
123	GlyAlaAlaAlaThrThrAlaSerAsnThrAlaThrLysIleAlaMetGlnThrSerIle	104	ДУ
360		301	
103	uSerSerGluSerGlnLysAlaGlyAlaAspThrGlyValSer	84	Qy
		241	Db
83	aSerGlyLysAspLysThrSerSerThrThrLysThrGluThrAlaProGlnGlnGly	64	Оу
240		181	
180	ATACAGCAAACACGTCAGGGTAAAAACACTGAGATGGAAAGCGATGCCACTATTGCTGGT	121	Db

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84 ValAlaAlaGlyLysGluSerSerGluSerGlnLysAlaGlyAlaAspThrGlyValSer 103
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                                                                                                                                                                               L Patent: JP 1997015244-A 1 17-JAN-1997;
HITACHI CHEM CO LTD
SC Chlamydia pneumoniae
PN JP 1997015244-A/1
PD 17-JAN-1997
PF 14-MAR-1996 JP 1996057410
PR 28-APR-1995 JP 95P 106011
PI IZUTSU HIROSHI, MATSUMOTO AKIRA
PC G01N33/571,C07K14/295,C07K16/12,G01N33/53,
PC G01N33/571,C07K14/295,C07K16/12,G01N33/53,
PC G01N33/569/A61K49/00,C12N15/09;
CC strandedness: Double;
CC topology: Linear;
FH Key Location/Qualifiers
FH Key Course 1..1464
FT source 1..1464
                                                                           ThrSerThrProGlnGlyValProGlnGlnAspLysLeuSerGlyAsnGluThrLysGln 43
                          AlaSerGlyLysAspLysThrSerSerThrThrLysThrGluThrAlaProGlnGlnGly 83
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1 IZUTSU, H. and Matsumoto, A.

MEASURING METHOD FOR ANTICHLAMYDIA-PNEUMONIA ANTIBODY AND REAGENT THEREFOR AS WELL AS DIAGNOSTIC MEDICINE FOR CHLAMYDIA PNEUMONIA
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encoding an antigen peptide Chlamydia pneumoniae.
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/product='antigen peptide'.
Location/Qualifiers
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/db_xref="taxon:32644"
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	GTCGCTCAATTTCAGAAAGAAGTCGGAAAACTGCAGGCTGCGGCTGATATGATTTCTATT	1261	DЬ
t 443	alAlaGlnPheGlnLysGluValGlyLysLeuGlnAlaAlaAlaAspMetIleScrMe	424	Qy
in 423    C 1260	AlaAlaProAlaLeuGlyLysGlyIleMetGlnMetGlnLeuSerGluMetGlnAs:	404 1201	Qу
	CGAAAGTCATCTCGTCTCTTACCAGTAAATGGGTCACGGTTGGGGTTGGGGTTGTAGT	1141	Db
1 403	ValThrValGlyValGlyValValVa	384	Qy
C 1140	GGAATCTCTAAGGTTTTCGCTAAGGGAACTCAAATGATTGCGAAGACTTCCCCAAGCT	1081	Db
eu 383	lyIleSerLysValPheAlaLysGlyThrGlnMetIleAlaLysAsnPheProLysLe	364	Qy
A 1080	TCTGGAATAAAAGCATTTATCAAAACTTTAGTCAAAGCGATTGCCAAAGCCATTTCTAA	1021	Db
/s 363	erGlyIleLysAlaPheIleLysThrLeuValLysAlaIleAlaLysAlaIleSerLy	344	Qy
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/s 343	lnalavalIleThralavalargGlnalaIleThralaalaIleLysalaalaValLy	324	Qy
1 A 96	GCTGCCGCAACCACGGTAGCAACACACAAATTACAGTTCAAGCTGTTGTCCAAGCGGTGAA		Db
s ω	LaAlaAlaThrThrValAlaThrGlnIleThrValGlnAlaValValGlnAlaValLy	304	Qy
T 9	GCTGGACTCGCTGCGGGAGCTGCTGTAGGTGCAGCGGCAGCTGGAGGTGCAGCAGGAGC	841	Db
la 303	laGlyLeuAlaAlaGlyAlaAlaValGlyAlaAlaAlaAlaGlyGlyAlaAlaGlyAl	284	Qy
ω -	TCTGTTGCCATTACAGTTATTTCTATTGCTGCTATTTTTACATGCGGAGCTGGACT	781	Дb
28	erValAlaIleThrValIleSerIleValAlaAlaIlePheThrCysGlyAlaGlyI	264	Qy
œ		721	Db
2	lnLysSerLysAspLeuGluGlyThrMetAspThrValAsnThrValMetIleAlav	244	Qy
	AAGCAAGCGATAAAAATCGATAAAGAACGAGAAGAATACCAAGAGATGAAGGCTGCCGA	661	Db
lu 243	ysGlnAlaIleLysIleAspLysGluArgGluGluTyrGlnGluMetLysAlaAlaC		Qy
A –	TTATCTAACTATGCAAGTACACAAGCACAAGCAGACCAAACAAA	601	Db
lu 223	euSerAsnTyrAlaSerThrGlnAlaGlnAlaAspGlnThrAsnLysLeuGlyLeuG	204	Qy
ი <del>–</del>	GAAATCGGACTCGCGCTTGCTAAAGCAATTCAGACATTGGGAGAAGCCACAAAATCTGC	541	Db
la 203	luileGlyLeuAlaLeuAlaLysAlaIleGlnThrLeuGlyGluAlaThrLysSerA	184	Qy
4.	GCAAAATTGGAAACACCTGAGCTCCCCAAGCCCGGGGTGACACCAAGATCAGAGGTTAT	481	Дb
e 1	laLysLeuGluThrProGluLeuProLysProGlyValThrProArgSerGluValI	164	Qy
	CAAATGAAAGAAGTCGAAGCGGTTGTTGTTGCTGCCCTCTCAGGGAAAAGTTCGGGTTC	421	Db
	lnMetLysGluValGluAlaValValValAlaAlaLeuSerGlyLysSerSerGlyS	144	Qy
[] CG 420	GAAGAGGCGAGCAAAAGTATGGAGTCTACCTTAGAGTCACTTCAAAGCCTCAGTGCCGC	361	Db
	luGluAlaSerLysSerMetGluSerThrLeuGluSerLeuGlnSerLeuSerAlaA	124	QΥ
le 123  - TT 360	GlyAlaAlaAlaThrThrAlaSerAsnThrAlaThrLysIleAlaMetGlnThrSerI:	301	ду Ду
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                                                                                                       GlyAlaAlaAlaThrThrAlaSerAsnThrAlaThrLySIleAlaMetGlnThrSerIle
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12UTSU HIROSHI, MATSUWOTO AKIRA
C12Q1/68,C07H21/04,C12N1/21,C12N15/02,C12N15/09,C12P21/08,
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Location/Qualifiers
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RS IZULESU, H. and MATSUMOLO, A.

RRS IZULESU, TRANSFORMANT

CONTAINING THE VECTOR, CONTAINING THE DNA, TRANSFORMANT

CONTAINING THE VECTOR, AND PRODUCTION OF ANTI-CHLAMYDIA PNEUMONEAE

PACENTAINING THE VECTOR ANTI-CHLAMYDIA PN
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                                             GlyAlaAlaAlaThrThrAlaSerAsnThrAlaThrLysIleAlaMetGlnThrSerIle
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	SerGlyAlaILeAlaGlyAla	148	P &
1440	GAAATGACTCAAAAAGCTACCAAGCTGGGCGCTCAAATCCTTAAAGCGTATGCCGCAAT	a	00
	4 GluMetThrGlnLysAlaThrLysLeuGlyAlaGlnIleLeuLysAlaTyrAlaAlaIle	6	Qy
· ω		132	Db .
ωi	heThrGlnPheTrpGlnGlnAlaSerLvsIleAlaSerLvsGlnThrGlvGluSerAs	44	ο ν
443 1320	VALALAGI, ILPAGI, LIVESGI, LIVESGI, VESSIGUI, LIA LA LA LA SPAGITI LESET MET 		Db 49
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2 2	4 AlaAlaProAlaLeuGlyLySGlyILeMetGlmMetGlmLeuSerGluMetGlmGlmAsn	2 6	P 04
	TCGAAAGTCATCTCGTCTTACCAGTAAATGGGTCACGGTTGGGGTTGGGGTTGTAGT	4	gd
403	4 SerLysVallleSerSerLeuThrSerLysTrpValThrValGlyValGlyValValValValValValValValValValValValValV	38	Qy
1140	GAATCTCTAAGGTTTTCGCTAAGGGAACTCAAATGATTGCGAAGAACTTCCCCCAAGCT		Db
383	GlyIleSerLysValPheAlaLysGlyThrGlnMetIleAlaLysAsnPheProLysLeu	6	Qy
1080	CTGGAATAAAAGCATTTATCAAAACTTTAGTCAAAGCGATTGCCAAAGCCATTTCTAA	N	DЬ
363	SerGlyIleLysAlaPheIleLysThrLeuValLysAlaIleAlaLysAlaI	4	QУ
1020	TGTTATCACAGCTGTCAGACAAGCGATCACCGCGGCTATAAAAG	96	DЬ
343	lnAlaValIleThrAlaValArgGlnAlaIleThrAlaAlaIleLysAlaAlaValLy	N	Qy
		0	Db
323	laAlaAlaThrThrValAlaThrGlnIleThrValGlnAlaValValGlnAlaValLy	30	Qy
900	CGGGAGCTGCTGTAGGTGCAGCGG	84	Db
303	laGlyLeuAlaAlaGlyAlaAlaValGlyAlaAlaAlaAlaGlyGlyAlaAlaGlyAl	œ	Qy
840	TTATTTCTATTGTTGCTGC	æ	DЬ
283	erValAlaIleThrValIleSerIleValAlaAlaIlePheThrCysGlyAlaGlyLe		Qy
780	TGGATACTGTCAATACTGTGATGATCGC	72	Дb
263	lnLysSerLysAspLeuGluGlyThrMetAspThrValAsnThrValMetIleAlaVa	24	Qy
	GCGATAAAATCGATAAAGAACGAGAAGAATACCAAGAGATGAAGGCTGC	66	Дb
243	ysGlnAlaIleLysIleAspLysGluArgGluGluTyrGlnGluMetLysAlaAlaGl	N	Qy
660	AACTATGCAAGTACACAAGCACAAGCAGACCAAACAAATAAACTAGGT	60	Db
223	LeuSerAsnTyrAlaSerThrGlnAlaGlnAlaAspGlnThrAsnLysLeuGlyLeuGl	0	Qy
600	AATTCAGACATTGGGAC	54	Db
203	uIleGlyLeuAlaLeuAlaLysAlaIleGlnThrLeuGlyGluAlaThrLysSerAl	œ	Qy
540	CAAGCCCGGGGTGACAC	48	DЬ
183	laLysLeuGluThrProGluLeuProLysProGlyValThrProArgSerGluValIl	16	Qy
480	1 CAAATGAAAGTAGTCGAAGCGGTTGTTGTTGTCCTCCTCAGGGAAAAGTTCGGGTTCC	42	Дb

RESULT 13 E12535

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BASE COUNT
ORIGIN
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GluIleGlyLeuAlaLeuAlaLysAlaIleGlnThrLeuGlyGluAlaThrLysSerAla
                    AlaLysLeuGluThrProGluLeuProLysProGlyValThrProArgSerGluValIle 183
                                                             GluGluAlaSerLysSerMetGluSerThrLeuGluSerLeuGlnSerLeuSerAlaAla 143
                                                                                                                                                             GlyAlaAlaAlaThrThrAlaSerAsnThrAlaThrLysIleAlaMetGlnThrSerIle 123
                                                                                                                                                                                          GTTGCTGCTGGGAAAGAATCCTCAGAAAGTCAAAAGGCAGGTGCTGATACTGGAGTATCA
                                                                                                                                                                                                    ValAlaAlaGlyLysGluSerSerGluSerGlnLysAlaGlyAlaAspThrGlyValSer 103
                                                                                                                                                                                                                                               AlaSerGlyLysAspLysThrSerSerThrThrLysThrGluThrAlaProGlnGlnGly 83
                                                                                                                                                                                                                                                                              IleGlnGlnThrArgGlnGlyLysAsnThrGluMetGluSerAspAlaThrIleAlaGly 63
                                                                                                                                                                                                                                                                                                                      ThrSerThrProGlnGlyValProGlnGlnAspLysLeuSerGlyAsnGluThrLysGln 43
                                                                                                                                                                                                                                                                                                                                                                 ATCAGCGGAGCCATCGCTGGCGCA 1584
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                                                                                                                                                                                                                                     GCTTCTGGAAAAGACAAAACTTCCTCGACTACAAAAACAGAAACAGCTCCACAACAGGGA
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                                                                                                        GAAGAGGCGAGCAAAAGTATGGAGTCTACCTTAGAGTCACTTCAAAGCCTCAGTGCCGCG
                                                                                                                                                  GGAGCGGCTGCTACTACAGCATCAAATACTGCAACAAAAATTGCTATGCAGACCTCTATT
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Sequence
AR122105
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Izutsu,H., Obara,K. and Matsumoto,A.
DNA encoding Chlamydia pneumoniae antigenic
Patent: US 6165478-A 3 26-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unknown
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patent US 6165478.
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KEYWORDS SOURCE DEFINITION ACCESSION VERSION

ъ 5	41		
2y 2 5b 6	04	LeuSerasnTyralaSerThrGlnAlaGlnAlaAspGlnThrAsnLysLeuGlyLeuGlu 223 	
2у 2	24	ysGlnAlaIleLysIleAspLysGluArgGluGluTyrGlnGluMetLysAlaAlaG	
9 qc	61	AAGCAAGCGATAAAAATCGATAAAGAACGAGAGAAGAATACCAAGAGATGAAGGCTGCCGAA 720	
2у 2 Эь 7	21	GlnLysSerLysAspLeuGluGlyThrMetAspThrValAsnThrValMetIleAlaVal 263 	
2γ 2	64	SerValAlaIleThrValIleSerIleValAlaAlaIlePheThrCysGlyAlaGlyLeu 283	
Ob 7	81	CTGTTGCCATTACAGTTATTTCTATTGTTGCTGCTATTTTTACATGCGGAGCTGGAC	
	84	0	
9 0 0	41	CTGGACTCGCTGCGGGAGCTGCTGGTAGGTGCAGCGGCAGCTGGAGGTGCAGCAGGAGC	
2y 3 0b 9	04	AlaAlaAlaThrThrValAlaThrGlnIleThrValGlnAlaValValGlnAlaValLys 323 	
Σγ з	24	lnAlaValIleThrAlaValArgGlnAlaIleThrAlaAlaIleLysAlaAlaVal	
9	61	AGCTGTTATCACAGCTGTCAGACAAGCGATCACCGCGGCTATAAAAAGCGGCTGTCA	_
Dy 3	44	SerGlyIleLysAlaPheIleLysThrLeuValLysAlaIleAlaLysAlaIleSerLys 363	-
ΩУ	64	lylleSerLysValPheAlaLysGlyThrGlnMetIleAlaLysAsnPheProLysLe	
Db 10	81	TCTCTAAGGTTTTCGCTAAGGGAACTCAAATGATTGCGAAGAACTTCCCCAA	_
	84	03	
Db 11	41	CGAAAGTCATCTCGTCTCTTACCAGTAAATGGGTCACGGTTGGGGGTTGGGGTTGTAGT	Ŭ
2y 4 Db 12	04	AlaAlaProAlaLeuGlyLysGlyIleMetGlnMetGlnLeuSerGluMetGlnGlnAsn 423 	_
2y 4 Db 12	24 61	ValAlaGlnPheGlnLySGluValGlyLySLeuGlnAlaAlaAlaAspMetIleSerMet 443 	-
2γ 4	44	heThrGlnPheTrpGlnGlnAlaSerLysIleAlaSerLysGlnThrGlyGluSerAs	
Db 13	21	TTCACTCAATTTTGGCAACAGGCAAGTAAAATTGCCTCAAAACAAAC	_
	64	83	
,		CHICA CHERENOCANOCANOCANOCA CHERA COA LIBRIDOCATA COCANA	
2y 4 Db 14	84 41	SerGlyAlaIleAlaGlyAla 490 	
RESULT E12520 LOCUS DEFINIT ACCESSION VERSION KEYWORD	s or r	E12520 1464 bp DNA linear PAT 27-APR DNA encoding an antigen peptide of Chlamydia pneumoniae. E12520 E12520.1 GI:3251353 JF 199709974-A/1. unidentified.	199
Ř	MSI	nidentified nclassified	

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TITLE
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  103
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                                                                                                                                                                                    GlyValAlaAlaGlyLysGluSerSerGluSerGlnLysAlaGlyAlaAspThrGlyVal 102
                                                                             GlnIleGlnGlnThrArgGlnGlyLysAsnThrGluMetGluSerAspAlaThrIleAla
SerGlyAlaAlaAhaThrThrAlaSerAsnThrAlaThrLysIleAlaMetGlnThrSer 122
                          GGAGTTGCTGGGAAAGAATCCTCAGAAAGTCAAAAGGCAGGTGCTGATACTGGAGTA
                                                                                                                                  CAAATACAGCAAACACGTCAGGGTAAAAACACTGAGATGGAAAGCGATGCCACTATTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent: JP 198212298
HITACHI CHEM CO LTD
OS
OC Artificial seque
PN JP 198212298-A/
PD 11-AUG-1998
PF 31-JAN-1997 JP 1
PI IZUTSU HIROSHI,
PC C07K16/12,C07K19
C12P21/08,
PC G01N33/531,G01N3
PC (C12P21/08,C12R1
CC Strandedness: Dc
CC topology: Linear
CC hypothetical: No
CC anti-sense: No;
FH Key
FT source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   I (bases 1 to 1587)
IZUTSU,H. and Hagiwara,T.
IZUTSU,H. and Hagiwara,T.
IZUTSU,H. and Hagiwara,T.
IZUTSU,H. and Hagiwara,T.
ITSURO PROPERTIES FUSION PROTEIN, PRODUCTION, DNA CODING FOR THE SAME FUSION PROTEIN, RECOMBINANT VECTOR CONTAINING THE DNA, TRANSFORMANT CONTAINING THE CHECOMBINANT VECTOR, RECOMBINANT BACULOVIRUS, ITS PRODUCTION AND PRODUCTION OF ANTI- CHLANYDIA PNEUMONIAE ANTIBODY
PATENT: JP 1998212298-A 1 11-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polypeptide fused protein.
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31-JAN-1997 JP 1997018522
IZUTSU HIROSHI, HAGIWARA TOSHIKATSU
C07K16/12,C07K19/00,C12N5/10,C12N7/00,C12N15/09,C12P21/02,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Artificial sequences.
JP 1998212298-A/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G01N33/531,G01N33/571//A61K39/395,C07K14/295,(C12N5/10, PC
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Location/Qualifiers
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363 c 384 g 3
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482	AsnGluMetThrGlnLysAlaThrLysLeuGlyAlaGlnIleLeuLysAlaTyrAlaAla	463	Qy
1500	TGTTCACTCAATTTTGGCAACAGGCAAGTAAAATTGCCTCAAAACAAAC	4	Дb
462	MetPheThrGlnPheTrpGlnGlnAlaSerLysIleAlaSerLysGlnThrGlyGluSer	443	VQ
442	lGlyLysLeuGlnAlaAlaAspMetIleSer	423	дь
1440		1381	Оу
	AlaAlaProAlaLeuGlyLysGlyTleMetGlnMetGlnLeuSerGluMetGlnGln 	20	Фр
402	SValIleSerSerLeuThrSerLysTrpValT	383	Db
1320		1261	Db
382 1260	IleAlaLysAsnPheProLys             ATTGCGAAGAACTTCCCCAAG	363 1201	ДУ
	SerGlyIleLysAlaPheIleLysThrLeuValLysAlaIleAlaLysAlaIleSer 		Qу
342	LysGlnAlaValIleThrAlaValArgGlnAlaIleThrAlaAlaIleLysAlaAlaVal	323	Оу
1140		1081	Db
322 1080	hrThrValAlaThrGlnIleThrValGlnAlaValValGlnAlaVal 		Оу
302	AlaG1yAlaAlaValG1yAlaAlaAlaAlaG1yG1yAlaAlaG1y	283	Qy
1020		961	Db
282	eThrVallleSerIleValAlaAlaIlePheThrCysGlyAlaGly	263	Оу
960		901	
262	uGlnLysSerLysAspLeuGluGlyThrMetAspThrValAsnThrValMetIleAla	243	Qy
900		841	Db
242 840	leAspLysGluArgGluGluTyrGlnGluMetLysAlaAla 	223 • 781	Оу
222	AsnTyrAlaSerThrGlnAlaGlnAlaAspGlnThrAsnLysLeuGlyLeu	203	Qy
780		721	Db
202	eGluIleGlyLeuAlaLeuAlaLysAlaIleGlnThrLeuGlyGluAlaThrLysSer	183	Qy
720		661	Db
182	SerAlaLysLeuGluThrProGluLeuProLysProGlyValThrProArgSerGluVal	163	Qy
660		601	Db
162 600	AlaGlnMetLysGluValGluAlaValValValAlaAlaLeuSerGlyLysSerSerGly		Qy Db
142	LeuGluSerLeuGlnSerLeuSerAla	123	Qy
540		481	Db
480	TCAGGAGCGGCTGCTACACAGCATCAAATACTGCAACAAAAATTGCTATGCAGACCTCT	421	Db

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BASE COUNT
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Best Local Similarity:
Query Match:
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PD 11-AUG-1998

PF 31-JAN-1997 JP 1997018522

PF 12UTSU HIROSHI, HAGIWARA TOSHIKATSU

PC C07K16/12,C07K19/00,C12N5/10,C12N7/00,C12N15/09,C12P21/02,C12P21/08,

PC G01N33/531,G01N33/571/A61K39/395,C07K14/295,(C12N5/10, PC C12P21/02,C12R1:91);

PC (C12P21/02,C12R1:91);

CC strandedness: Double;

CC topology: Circular;

FH Key Location/Qualifiers

FH Key 1..11099

FT source 1..11099

A135..5601
                                                                                                                               GlnIleGlnGlnThrArgGlnGlyLysAsnThrGluMetGluSerAspAlaThrIleAla
GlyAlaSerGlyLysAspLysThrSerSerThrThrLysThrGluThrAlaProGlnGln
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C07K16/12,C07K19/00,C12N5/10,C12N7/00,C12N15/09,C12P21/02,
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10 E16671 1587 bp DNA linear PAT 28-JUL-199 ION DNA encoding histidine tag - Chlamydia pneumoniae antigen	83 IleSerGlyAlaIleAlaGlyAla-HisLysThrAsnAsn 495 	63 AsnGluMetThrGlnLysAlaThrLysLeuGlyAlaGlnIleLeuLysAlaTyrAlaAla 482	43 MetPheThrGlnPheTrpGlnGlnAlaSerLysIleAlaSerLysGlnThrGlyGluSer 462 	23 AsnValAlaGlnPheGlnLysGluValGlyLysLeuGlnAlaAlaAlaAspMetIleSer 442 	03 ValAlaAlaProAlaLeuGlyLysGlyIleMetGlnMetGlnLeuSerGluMetGlnGln 422 	83 LeuSerLysvall1eSerSerLeuThrSerLysTrpValThrValGlyValGlyValVal 402 	53 LysGlyIleSerLysValPheAlaLysGlyThrGlnMetIleAlaLysAsnPheProLys 382 	13 LysSerGlyIleLysAlaPheIleLysThrLeuValLysAlaIleAlaLysAlaIleSer 362 	23 LysGlnAlaValIleThrAlaValArgGlnAlaIleThrAlaAlaIleLysAlaAlaVal 342 	32 AlaAlaAlaAlaThrThrValAlaThrGlnIleThrValGlnAlaValValGlnAlaVal 322 	33 LeuAlaGlyLeuAlaAlaGlyAlaAlaValGlyAlaAlaAlaGlyGlyAlaAlaGly 302 	33 ValSerValAlaIleThrVallleSerIleValAlaAlaIlePheThrCysGlyAlaGly 282 	3  GluGlnLysSerLysAspLeuGluGlyThrMetAspThrValAsnThrValMetIleAla 262 	3 GluLysGlnAlaIleLysIleAspLysGluArgGluGluTyrGlnGluMetLysAlaAla 242 	33 AlaLeuSerAsnTyrAlaSerThrGlnAlaGlnAlaAspGlnThrAsnLysLeuGlyLeu 222 	33 IleGluIleGlyLeuAlaLeuAlaLysAlaIleGlnThrLeuGlyGluAlaThrLysSer 202 	3 SerAlaLysLeuGluThrProGluLeuProLysProGlyValThrProArgSerGluVal 182 

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                               GluLysGlnAlaIleLysIleAspLysGluArgGluGluTyrGlnGluMetLysAlaAla
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                     GAAAAGCAAGCGATAAAAATCGATAAAGAACGAGAAGAATACCAAGAGATGAAGGCTGCC
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Location/Qualifiers
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/db_xref="taxon:32644"
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All sequences of plass antigen polypeptide-cc E16677
E16677.1 GI:5711360
JP 1998212298-A/7.
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Izutsu,H. and Hagiwara,T.

HISTIDINE TAG CHLAMYDIA PNEUMONIAE ANTIGEN POLYPEPTIDE FUSION PROTEIN, ITS PRODUCTION, DNA CODING FOR THE SAME FUSION PROTEIN, RECOMBINANT VECTOR CONTAINING THE DNA, TRANSFORMANT CONTAINING TREOMBINANT PACULOVIRUS, ITS PRODUCTION AND PRODUCTION OF ANTI- CHLAMYDIA PNEUMONIAE ANTIBODY PATENT: JP 1998/112298-A 7 11-AUG-1998;
 HITACHI CHEM CO
OS None
OC Artificial
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                                                                                                                        ValSerValAlaIleThrValIleSerIleValAlaAlaIlePheThrCysGlyAlaGly
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                               AlaAlaAlaAlaThrThrValAlaThrGlnIleThrValGlnAlaValValGlnAlaVal
                                                                   CTCGCTGGACTCGCTGCGGGAGCTGCTGTAGGTGCAGCGGCAGCTGGAGGTGCAGCAGGA
                                                                            LeuAlaGlyLeuAlaAlaGlyAlaAlaValGlyAlaAlaAlaAlaAlaGlyGlyAlaAlaGly
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LysGlnAlaValIleThrAlaValArgGlnAlaIleThrAlaAlaIleLysAlaAlaVal
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All sequences of p
taq - Chlamydia F
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OS Artific
PN JP 1998
PD 11-AUG-
PF 31-TAUG-
PF 31-TAUG-
PF 31-TAUG-
PF GOT/K16,
C12P21/P,
PC GO1N33,
C12R1:91),
PC (C12P2
CC strand
CC topolo
CC hypoth
CC anti-s
FH Key
FH Source
FT Source
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1 (bases 1) to 9595)
1 IZUTSU, H. and Hagiwara, T.
1 IZUTSU, H. and Hagiwara, T.
1 IZUTSU, H. TAG CHLAMYDIA PNEUMONIAE ANTIGEN POLYPEPTIDE FUSION PROTEIN, ITS PRODUCTION, DNA CODING FOR THE SAME FUSION PROFEIN, RECOMBINANT VECTOR CONTAINING THE DNA, TRANSFORMANT CONTAINING TO RECOMBINANT VECTOR, RECOMBINANT BACULOVIRUS, ITS PRODUCTION AND PRODUCTION OF ANTI- CHLAMYDIA PRUBHONIAE ANTIBODY PATENT: JP 1998/12298-A 8 11-AUG-1998;
HITACHI CHEM CO LTD
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E16678.1 GI:57113
JP 1998212298-A/8.
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                                                   2676
                                                                                                                                                                                                                                                                                                                      strandedness: Double
topology: Circular;
hypothetical: No;
anti-sense: No;
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                                                                                                                                                                                                                                                                                                                                                                                                                             11-AUG-1998
31-JAN-1997 JP 1997018522
1ZUTSU HIROSHI, HAGIWARA TOSHIKATSU
C07K16/12,C07K19/00,C12N5/10,C12N7/00,C12N15/09,C12P21/02,
                                                                                                                    promoter
                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Artificial sequences JP 1998212298-A/8
                                                                                                                                                                                                                                                                                  source
                                                                                                                                                                                                                                                                                                                                                                            (C12P21/02,C12R1:91);
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2114 c 2191 g 261
                                                                                           Location/Qualifiers
1, .9595
                                                                                                                                baculovirus
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                                                                                                                                                                                                   polypeptide fused
1. .2128
                                                                                                                    2129. .2191
                                                                                                                                              /note='DNA
                                                                                                                                                              3868.
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                                                                                                                                                                                                                            antigen
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                                                                                                                                                                                                                                                                   organism='Artificial sequences'
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Length:

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SDTYIEKSLLINDEIDKLRLSATRSILERRDTLIVSSYSCIYGIGSPENYTSMALVLE
VGKEYERNILTAQLVKMHYQASPIPOKSAFRERGSVIDIFPAZESELALRLEFLNDTL
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                                                           FSHKWRSLLK"
                                                                                 EVKARLAEELIHFLKPIKERRSEFLSKPLALQNVLEDGTHKMREVAKVTMEEVHDKFG
                                                                                                             TITEKVRKMYTDPNRIRATTPGRVEGNPLFIYHDIFNPHKDEVEEFKARYRQGCIKDI
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SSKEKEQLRHLLQHYNFREQIEEPDLTQLCTLSAEVKQIHHQSVLLHGERITKVRDLL
KSYREGAFSSWLLLTYGNRQTPYNFLVYYELFTLLPEPLKIEMEKMPRQAVYTLASRQ
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RLAGFIQGISARHPLTILGVALSFWNCRGKNNSAFAELIHKTFPGKLLNTKIRRDITV
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HSTRTDGEYRAFKYVDGRMIDLGTLGGSASFAFGVSDDGKTIVGKFETELGECHAFIY
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GSIIVGVSATARGEDYGWQVGVKWEKGKIKQLKLLPQGLWSEANAISEDGTVIVGRGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="synonym:Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .325865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chlamydiales; Chlamydiaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ∕organism="Chlamydophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ocation/Qualifiers
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pneumoniae J138
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/protein_id="ABF38836.1"

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/db_xref="GI:7189977"

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KASFOSONATHSQVESAPAICEAIKRQANGASTEAPAKOSLISGITVLYGGTVSV
KASFOSONATHSQVESAPAICEAIKRQANGASTEAPAKOSLISGITVLYGGTVSV
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ASSAGSAATKAAANLTDDMAAAASKMASDGASKALTSASGCLFGEVLKFNWSEKVSRGMNV
VETOCABEVRSSENANG
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AKLETPELFRCOVTPRSEVIETGLALAKAIQTIGEATWSALSNVASTQAADOTKKLG
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                                                                                                                                                                                                     /gene="CP1065"
8288. .10195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="membrane protein, PFAM protein family HMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(7177. .8094)
/gene="CP1064"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AEVLKOMSSYVGQQAGQAGQLQEQAMQSFNTALQTLQNIADSQTQTTSAIFN" complement(7177. .8094)
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Glimmer2; putative"
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5772. .7106
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TVGVGVVVAAPALGKGIMQMQLSEMQQNVAQFQKEVGKLQAAADMISMFTQFWQQASK
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4273. .5739
                                                                                                                PID:1565235 GB:AL009126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="membrane protein, putative"
/protein_id="AAF73728.1"
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LPLAQTFASLTDKNQINSIIAALSGTLESLHLEELTQGLFPSAQEDANFAKELSSVVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="conserved hypothetical protein"
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/db_xref="GI:7189975"
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/transl_table=11
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                                                                                                                                                                    /gene="CP1065"
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                                                                                                                                            /note="similar to GB:M36593 SP:P18256 PID:143764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /transl_table=11
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/product="threonyl-tRNA synthetase"
                                                                                                                                                                                                                                                                                           LGLVLAVAFMVAGCRLIYHEEFRQGYIVS"
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Pred. No.:
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SerGlySerAlaLysLeuGluThrProGluLeuProLysProGlyValThrProArgSer 180
                                                                                                                                ThrSerIleGluGluAlaSerLysSerMetGluSerThrLeuGluSerLeuGlnSerLeu 140
                                                                                                                                                                                                                                                                                                                        IleAlaGlyAlaSerGlyLysAspLySThrSerSerThrThrLySThrGluThrAlaPro
                                                                                                                                                                                                                                                                                                                                                                                                                                    CAAGTTCTGACATCGACACCCCAGGGGCGTGCCCCAACAAGATAAGCTGTCTGGCAACGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scores:
                                                AGTGCCGCGCAAATGAAAGAAGTCGAAGCGGTTGTTGTTGCTGCCCCTCTCAGGGAAAAGT
                                                                              SerAlaAlaGlnMetLysGluValGluAlaValValAlaAlaLeuSerGlyLysSer 160
                                                                                                              ACCTCTATTGAAGAGGCGAGCAAAAGTATGGAGTCTACCTTAGAGTCACTTCAAAGCCTC
                                                                                                                                                                                                                                                                                                         ATTGCTGGTGCTTCTGGAAAAGACAAAACTTCCTCGACTACAAAAACAGAAACAGCTCCA
                                                                                                                                                                                                                                                                                                                                                                       ACGAAGCAAATACAGCAAACACGTCAGGGTAAAAACACTGAGATGGAAAAGCGATGCCACT
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/gene="CP1066"
10228. .10995
/gene="CP1066"
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GB:AL009126; identified by sequence similarity;
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Indels:
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Submitted (01-MAR-2000) The Institute for Genomic Research,
Madical Center Dr. Rockville, MD 20850, USA
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On Jun 1, 2000 this sequence version replaced gi:7189971
    /note="conserved hypothetical protein; identified by
Glimmer2; putative"
/codon_start=1
                                                                                                                                       3874.
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3158. .3853
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="similar to GP:3372642;
similarity; putative"
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/gene="CP1058"
/gene="CP1058"
.1188)
                                                                                                                                                              SKTTTNKKSGKKR"
                                                                                                                                                                                  KLQQPEESNNFLDVTMDICGNNPEFKILKERCQIMKQSIEKQMAGETKKAPTKKPAGK
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/db_xref="GI:7189973"
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/transl_table=11
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                                                                   /gene="CP1061"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GluSerAsnGluMetThrGlnLysAlaThrLysLeuGlyAlaGlnIleLeuLysAlaTyr
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PN JP 199
PD 11-AUG
PF 31-JAW
PI 12UTSU
PC CO7K16
C12P21/08,
PC G01N33
C12R1:91),
PC (C12P2
CC strand
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CC anti-s
FH Key
FH Key
FH Source
FT Source
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Ghamencoding Chlamydia

E16674

E16674.1 GI:5711357
                                                                                                                                                                                                                                                         IZULSU,H. and Hagiwara,T.

HISTIDINE TAG CHLAMYDIA PNEUMONIAE ANTIGEN POLYPEPTIDE FUSION PROTEIN, ITS PRODUCTION, DNA CODING FOR THE SAME FUSION PROTEIN, RECOMBINANT VECTOR CONTAINING THE DNA, TRANSFORMANT CONTAINING TRECOMBINANT VECTOR, RECOMBINANT BACULOVIRUS, ITS PRODUCTION AND PRODUCTION OF ANTI- CHLAMYDIA PREDUMONIAE ANTIBODY PALENCE, JP 1998/12298-A 4 11-AUG-1998;
HITAGHI CHEM CO LTD
                 F F F T
                                                                                                                                                                                                                                                                                                                                                           unclassified
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                                                                                                                                                                          G01N33/531,G01N33/571//A61K39/395,C07K14/295,(C12N5/10,
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31-JAN-1997 JF 1997018522
IZUTSU HIROSHI, HAGIWARA TOSHIKATSU
C07K16/12,C07K19/00,C12N5/10,C12N7/00,C12N15/09,C12P21/02,
                                                                                                                                                                                                                                       Chlamydia pneumoniae
JP 1998212298-A/4
                                                                                                                     topology: Linear;
hypothetical: No;
                                                                                                                                          strandedness: Double;
                                                                                                                                                      (C12P21/02,C12R1:91);
                                                     /organism='Chlamydia
/product='Chlamydia
                                                                                                             No;
                                                                                                   Location/Qualifiers
                          236. .1702
                                                /clone='53-35
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Location/Qualifiers
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| IleAlaValSerValAlaIleThrValIleSerIleValAlaAlaIlePheThrCysGly
                                                                                  AlaAlaGluGlnLysSerLysAspLeuGluGlyThrMetAspThrValAsnThrValMet
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                                                               GCTGCCGAACAGAAGTCTAAAGATCTCGAAGGAACAATGGATACTGTCAATACTGTGATG
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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100

466 80 406 60 346 40 286 20

526

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280

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Alignment
Pred. No.:
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 Best Local Similarity: Query Match:
DB:
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AUTHORS
TITLE
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E16639 GI:5711322
JP 1998210978-A/5.
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OS Chlamydia pneumc
PN JP 19821078-A
PD 11-AUG-1998
PF 31-ANT-1997 JP
PI IZUTSU HIROSHI
C12P21/02/
PC A61K39/00, A61K39
PC C12R1:19)
PC (C12N5/10,C12R1:
CC strandedness: Do
CC topology: Linear
FH Key
FT source
FT source
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RECOMBINANT VECTOR AND TRANSFORMANT CONTAINING THE SAME,
RECOMBINANT VACUROVIRUS AND ITS PRODUCTION, AND PRODUCTIC
CHLAMYDIA PNEUMONIAE ANTIGEN POLYPEPTIDE
PATENT: JP 1998210978-A 5 11-AUG-1998;
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IZUTSU HIROSHI, HAGIWARA TOSHIKATSU
C12N15/09,C07H21/04,C07K14/295,C12N1/21,C12N5/10,C12N7/00,
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                                                                                                                                                                                                                                                    strandedness: Double;
                                                                                                                                                                                                                                         topology: Linear;
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                                                                                                                                                                                  /organism='Chlamydia
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                                                                                                                               /product='53kDa-antigen
Location/Qualifiers
1. .1939
                                                                                                 /organism="unidentified"
/db_xref="taxon:32644"
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SOURCE
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
1 (bases 1 to 16903)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (01-DEC-1998) Program in Infectious Diseases, University of California, 235 Earl Warren Hall, Berkeley, CA 94720, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
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Kalman,S., Mitchell,W.,
Grimwood,J., Davis,R.W.
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Comparative
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1021 GCTGTCAAATCT	מס	(1-1491)	50-Sn : an
	Qy	Mismatches: Indels:	Best Query
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	da s	Location/Qualifiers	FEATURES sou
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181 GluValīleGlu	Оу	AUTHORS Matthews, R.C. and Burnie, J.P. TITLE Medicament	AUT
161 SerGlySerAla 	Оу	Chl NISM Chl Bac	SOURCE ORGAI
	Db	N AX033283 AX033283	ACCESSIO VERSION KEYWORDS
361 ACCTCTATTGAA	EP-2000 Db	283 ITION	AX033283 LOCUS DEFINITI

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GenCore version 5.1.3 Compugen Ltd

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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Y
Fgapop 6.0 , F
Delop 6.0 , I
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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ALIGNMENTS

aGlyAlaHisLySThrAsnAsn 495 GGAGGCCAGGGCGGAGACTCC 2343		488 2322	Db Qy
GAGCTGAGTGGCCTCCACGGGCAGCTCCA 2321	ATGCGAGGAGCTG-	2286	Db
SAlaThrLysLeuGlyAlaGlnIleLeuLysAlaTyrAlaAlaIleSerGlyAlaIleAl 488	sAlaThrLysLeuG	468	Qy
::::::::	GCAGCAGATGGCCG	2226	Db
pGlnGlnAlaSerLysIleAlaSerLysGlnThrGlyGluSerAsnGluMetThrGlnLy 468	pGlnGlnAlaSerL	448	Qy
GGGCAGCCACGCCAGCCTCCGGGCGGATGCCCGAGAAGGCCCCAGGAGCAACA 2225	  GGGCAGCCACGCCA	2175	Дb
Ala	nLysGluValGlyL	428	Qy
GAGTGAGGAGGCCCTGCAGAAGCGCCTGGACGAGGTCAGCCGGGAGCTGTGCCCACACGCA 2174	GAGTGAGGAGGCCC	2115	Дb
LeuSerGluMetGlnGlnAsnValAlaGlnPheGl 428		417	Qy
GAAGCCAAGGCAGCTGCCTTCGAGAAGCAGGTCCTGCAGCTGCAGGCGTCCCCACAGGGA 2114	GGAAGCCAAGGCAG	2055	Дb
lValValAlaAlaProAlaLeuGlyLysGlyIleMetGlnMetGln 416	lvalvalAlaAlap	401	Qy
CAAAGAGCTGGTGGAGAAGTCAGAGGCTGTGCGGCAAGATGAGCAGCAGCAGCGGAAAGCTCT 2054	CAAAGAGCTGGTGG	1995	рь
eSerSerLeuThrSerLysTrpValThrValGlyValGlyVa 401	eSerSerLeuThrS	387	Qy
GGTGGAGAGCAGAACGCAGAGCTGGCCAAGCTTCGGCAGGAGCTCAGCAAGGTCAG 1994	GGTGGAGAGCAAGC	1935	ДЪ
sValPheAlaLysGlyThrGlnMetIleAlaLysAsnPheProLysLeuSerLysValIl 387	sValPheAlaLysG	367	Qy
GGCCCGCCTGCAGCAGGAGACTCCATCCTGCGGGATGCCTTGAACCAGGCCACGAGCCA 1934	GGCCCGCCTGCAGC	1875	DЬ
AlaIleSerLysGlyIleSerLy 367		360	Qy
GCTGCAGGGCAAGATCCGGACTCTTCAGGAGCAGCTGGAGAATGGCCCCCAACACGCAGCT 1874	GCTGCAGGGCAAGA	1815	Db
yIleLysAlaPheIleLysThrLeuValLysAlaIleAlaLys 359	yIleLysAlaPheI	345	Qy
CACGGCTGTGCAGGCACGCATGCAGGCCAGCTACCGGGAGCACGTGAAGGAGGTGCAGCA 1814	CACGGCTGTGCAGG	1755	Db
eThralaValArgGlnAlaIleThrAlaAlaIleLysAlaAlaValLysSerGl 345	eThrAlaValArgG	327	Qy
AAAGTGAAAAAAGCAGCTGGTGGCCCGGGAGCAGGAGAT 1754	A	1717	DЬ
rThrValAlaThrGlnIleThrValGlnAlaValValGlnAlaValLysGlnAlaValIl 327	rThrValAlaThrG	307	Qy
GCAGCAGAAAAGGCCAAAGCAGCCGGGGAGGCC 1716	GCAGCAG	1681	Db
AlaAlaValGlyAlaAlaAlaAlaGlyGlyAlaAlaGlyAlaAlaAlaAlaTh 307	aAlaGlyAlaAlaV	287	Qy

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GCATCTGCATCGGCATCCGCATCTGCATCGGCGTCAGCATCGGCGTCAGCGTCG 1925539
                                                                                                                                                                GCGTCAGCATCCGCATCGGCGTCAGCATCAGCATCCGCATCGGCGTCAGCATCCGCATCG 1925419
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Percent Similarity: Best Local Similarity:

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                                           The specification describes an endogenous substrate for detecting herpes virus protease. Human p180 protein is specifically digested at the latter stage of the infection with Herpes virus protease, and so a substrate for this enzyme. The invention uses peptides comprising a cleavage site derived from human p180 protein. The substrate is used
                                                                                                                                                                              WPI; 200
P-PSDB;
                                                                                                                                                                                                                Goto
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Sequence 3725
                                                                                                                  Example 3; Page 44-46; 50pp; Japanese.
                                                                                                                                         Substrate for detecting herpes virus derived from human p180 protein -
                                                                                                                                                                                                                                                                01-MAR-2000; 2000JP-0060380
                                                                                                                                                                                                                                                                                       01-MAR-2001; 2001WO-JP01574
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GCGGCGAAAACGACAGGAACAACAGTGAAATCAGCATTAAAAAACAGGCTTTAGCGCTGTG
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                                                              The present invention relates to nucleic acid sequences (ABQ67188-ABQ71212) from Listeria sprobes equences are useful as probes and primers for identification and/or dhetection of Listeria (e.g. as contaminants in foods, or mutational analysis) and for analysis of gene expression. Proteins encoded by the nucleic acid sequences can be used to screen for compounds that modulate gene expression, replication and pathogenicity of Listeria (potential therapeutic agents), also for
anti-Listeria vaccines.
Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic
                                                 and pathogenicity of Listeria (potreating infections by Listeria,
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                                                                                                                                                                                                                                            New genomic sequences from Listeria species, useful treatment and prevention of infection, also related
                                                                                                                                                                                                                                                                                                                              Kunst F,
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AlaValValGlnAlaValLysGlnAlaValIleThrAlaValArgGlnAlaIleThrAla 336
                                                                                                                                                                   PheThrCysGlyAlaGlyLeuAlaGlyLeuAlaAlaGlyAlaAlaValGlyAlaAlaAla
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                                                                                                                                                                                                                                                                                                                                    GlnGluMetLysAlaAlaGluGlnLysSerLysAspLeuGluGlyThrMetAspThrVal
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                                            GCGTCTGAATCAGCATCAACGAGTGCATCAGCTTCAGCATCAACAAGTGCTTCAGCTTCA
                                                                                 AlaGlyGlyAlaAlaGlyAlaAlaAlaThrThrValAlaThrGlnIleThrValGln
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Mismatches:
Indels:
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                                                                         US-09-889-314-2 (1-496) x ABQ67197 (1-1163020)
                                                                                                             Query Match:
                                                                                                                          Percent Similarity:
Best Local Similarity:
                                                                                                                                                                            Alignment Scores
                          New genomic sequences from Listeria species, useful treatment and prevention of infection, also related antibodies and modulators \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABQ67197
                                                                                                                                                                                                                                                                                    The present invention relates to nucleic acid sequences (ABQ67188-ABQ71212) from Listeria sp. The sequences are useful as probes and primers for identification and/or detection of Listeria (e.g. as contaminants in foods, or mutational analysis) and for analysis of gene expression. Proteins encoded by the nucleic acid sequences can be used to screen for compounds that modulate gene expression, replication and pathogenicity of Listeria (potential therapeutic agents), also for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-OCT-2000; 2000FR-0012697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-OCT-2001; 2001WO-FR03061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Listeria innocua
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                                                                                                                                                                                                                                                                                                                                                                                         Claim 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kunst F,
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                                                                                                                                                               No.:
                                                                                                                                                                                                  Sequence 1163020 BP; 388339
                                                                                                                                                                                                                                       of the printed specification, but
                                                                                                                                                                                                                                                                           treating infections by Listeria, and are useful as immunogens
                                                                                                                                                                                                                           directly
                                                                                                                                                                                                                                                    Note: The sequence data for this patent did not form part
                                                                                                                                                                                                                                                                  anti-Listeria vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (INSP ) INST PASTEUR.
(CNRS ) CNRS CENT NAT
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                                                32 GlnGlnAspLysLeuSerGlyAsnGluThrLysGln----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard; DNA; 1163020
                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID 10; 180pp; French.
                                                                                                                                                                                                                           rinted specification, but was obtained in electronic fo
from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glaser
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{\tt IleGlnGlnThrArgGlnGlyLysAsnThrGluMetGluSerAspAlaThr}
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                      The present invention describes a computer readable medium which has the nucleotide sequences SEQ ID NO:1 to 391 (AAV52134 to AAV52524) recorded on it, or a representative fragment or a sequence at least 95% identical to SEQ ID NO: 1 to 391. The nucleotide sequences depicted in SEQ ID NO: 1 to 391 (AAV52524) are genomic fragments from Streptococcus pneumoniae. The present invention also describes an isolated nucleic acid molecule encoding a homologue of any of the regments of the S.pneumoniae genome (SEQ ID NO:1 to 391) where the nucleic acid molecule is produced by a process comprising: (a) screening a genomic DNA library using as a probe a target sequence defined by any of the sequences in SEQ ID NO:1 to 391, identifying members of the library which contain sequences that hybridise to the target sequence and isolating the nucleic acid molecules from the members; or (b) isolating mRNA, DNA or cDNA produced from an organism, amplifying nucleic acid
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at ftp.wipo.int/pub/published_pct_sequences.
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Mismatches: Indels: Matches: Conservative:

Query Match:

Best Local Similarity: Percent Similarity:

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Alignment
                                                                                                                                                                                                                                                The present invention describes a computer readable medium which has CC the nucleotide sequences SEQ ID NO:1 to 391 (AAV52134 to AAV52524) CC recorded on it, or a representative fragment or a sequence at least 95% CC identical to SEQ ID NO: 1 to 391. The nucleotide sequences depicted in CC SEQ ID NO: 1 to 391 (AAV52134 to AAV52524) are genomic fragments from CC streptococcus pneumoniae. The present invention also describes an CC isolated nucleic acid molecule encoding a homologue of any of the CC fragments of the S.pneumoniae genome (SEQ ID NO:1 to 391) where the CC nucleic acid molecule is produced by a process comprising: (a) screening CC a genomic DNA library using as a probe a target sequence defined by any CC of the sequences in SEQ ID NO:1 to 391, identifying members of the CC library which contain sequences that hybridise to the target sequence and CC isolating the nucleic acid molecules from the members; or (b) isolating CC molecules whose nucleotide sequence is homologous to amplification and isolating the amplified sequences. The computer CC the amplification and isolating the amplified sequences.
                                                                                                                                    Sequence
                                                                                                                                                                                  readable medium can be used in a computer-based system for identifying fragments of the S. pneumoniae genome of commercial importance, or expression modulating fragments of the S. pneumoniae genome. Products from the present invention can be used in diagnosis kits and assays, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 1383-1384; 1409pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Computer-readable medium with recorded Streptococcus pneumoniae polynucleotide sequences - useful in diagnostic kits and assays, and pharmaceutical compositions and vaccines for Streptococcus
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                         The present invention describes a computer readable medium which has CC the nucleotide sequences SEQ ID NO:1 to 391 (AAV52134 to AAV52524) CC recorded on it, or a representative fragment or a sequence at least 95% CC identical to SEQ ID NO:1 to 391. The nucleotide sequences depicted in CC SEQ ID NO:1 to 391 (AAV52134 to AAV52524) are genomic fragments from CC streptococcus pneumoniae. The present invention also describes an CC isolated nucleic acid molecule encoding a homologue of any of the CC fragments of the S.pneumoniae genome (SEQ ID NO:1 to 391) where the CC nucleic acid molecule encoding a brook of the 391) where the CC quencies in SEQ ID NO:1 to 391, identifying members of the S.pneumoniae genome (SEQ ID NO:1 to 391) where the CC isolating the nucleic acid molecules from the members or the target sequence and CC isolating the nucleic acid molecules from the members; or (b) isolating CC molecules whose nucleotide sequence is homologous to amplification primers derived from the fragment of the S. pneumoniae genome to prime CC readable medium can be used in a computer-based system for identifying fragments of the S. pneumoniae genome to prime CC expression modulating fragments of the S. pneumoniae, Products of from the present invention can be used in diagnosis kits and assays, and pharmaceutical compositions and vaccines for S. pneumoniae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AlaValValGlnAlaValLysGlnAlaValIleThrAlaValArgGlnAlaIleThrAla 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCAACAAGTACAAGCACGAGCGAATCCGATTCACAAAGCACATCATCATATACAAGTCAG
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     infection; immunisation; liver abscess;
                                                                                                             (first entry)
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                                                                                                                                                                                                                        DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    ----ATTGCAAGTGAGTCAGTATCGGAAAGTACATCAGAA
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     foot rot;
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US-09-889-314-2 (1-496) x AAI67640 (1-9726)
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DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores: Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention provides an isolated Fusobacterium necrophorum leukolpolypeptide and its truncated versions. The leukotoxin protein can expressed by standard recombinant methodology. The leukotoxin gene useful for preparing a vaccine which confers effective immunity againfection caused by F. necrophorum. The vaccine is useful for immunant an animal against liver abscesses caused by F. necrophorum and for preventing foot rot caused by F. necrophorum infection. The present
                                                                                                                                                            6761
                                                                                                                                                                                                                                                                                                                         6641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 10; Page 90-95; 108pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fusobacterium necrophorum polypeptide useful as vaccine in immunizing an animal against an infection e.g. foot rot, or liver abscesses caused
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bactericide; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9726 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence represents a DNA encoding a F. necrophorum full-length leukotoxin polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         by the bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-049245/06
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24-APR-2001;
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---GCCGGAGCTGGAATTCTTGCAGCCGGAGTATCTGGA-----GTGGTTTCTGTCAAT
                                     LysAlaGlyAlaAsp-----ThrGlyValSerGlyAlaAlaAlaThrThrAlaSer 111
                                                                               GAAAATGAGATAAAATCAGGTACTGGAATCGGTTCA
                                                                                                                                                                                                MetGluSerAspAlaThrIleAlaGlyAlaSerGlyLysAspLysThrSerSerThrThr
                                                                                                                                                                                                                                        GAGCTGGAATTGGAGCAGCAGTGGCAGTTACCAAAGATGAATCAAACACGAGAGCAAGAG
                                                                                                                   LysThrGluThrAlaProGlnGlnGlyValAlaAlaGlyLysGluSerSerGluSerGln
                                                                                                                                                          TG-AAAAATTCTAAAATTATGACT-----CGAAACAAGTTAGATGTAATAGCA
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2001US-0841786.
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Conservative:
Mismatches:
Indels:
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RESULT 37
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23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
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The
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                                                                                                                                                                                                                                                                                                                                                        AAS54978 standard; DNA; 7035
                 Claim 27;
                                 New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                      Haselbeck R,
Yamamoto RT,
                                                                                                               (ELIT-) ELITRA PHARM INC
                                                                                                                                         27-NOV-2000;
22-DEC-2000;
                                                                                                                                                                                                      21-MAR-2001; 2001WO-US09180
                                                                                                                                                                                                                       27-SEP-2001
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                                                                                                                                                                                                                                                         Staphylococcus
                                                                                                                                                                                                                                                                           antibiotic;
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invention relates to antisense inhibitors of genes essential
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                                                                     2001-611495/70
                                                             AAU37119
                 Seq
                                                                                                                                                                                                                                                                          ds; prokaryotic
;; antibacterial;
                                                                                                                                2000US-191078P.
2000US-206848P.
2000US-207727P.
2000US-242578P.
2000US-253625P.
2000US-257931P.
2001US-269308P.
                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                      Ohlsen
Xu HH;
                 ID No 8615; 511pp; English
                                                                                                                                                                                                                                                          aureus

    AATAGAGTAACTAGCCCTTCTAAAGGAATTGGAAGAAAATCAATGTC

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                                                                                               Zyskind JW,
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                                       - Of
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Alignment Scores: Pred. No.:
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3394
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                                                            US-09-889-314-2 (1-496) x AAI67647
                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention provides an isolated Fusobacterium necrophorum leukotoxin polypeptide and its truncated versions. The leukotoxin protein can be expressed by standard recombinant methodology. The leukotoxin gene is useful for preparing a vaccine which confers effective immunity against infection caused by F. necrophorum. The vaccine is useful for immunising
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                                                                                                                                                                                                                                                                                                           Sequence 11130
                                                                                                                                                                                                                                                                                                                                                                               preventing foot rot
sequence represents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fusobacterium necrophorum polypeptide useful as vaccine in immunizing an animal against an infection e.g. foot rot, or liver abscesses caused by the bacterium -
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                                                                                                                                                                                                                                                                                                                                                                                                      animal against liver abscesses caused by F, necrophorum and for eventing foot rot caused by F, necrophorum infection. The present
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                                                                 8639 GTAAATGTTAGATCGGATATTACAGGAAATGTTGCTTTAACAGCATATCAAGGTCCTGTA 8698
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AlaPheIleLysThrLeuValLysAlaIleAlaLysAlaIleSerLysGlyIleSerLys 367
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                                                                                             ThrAlaValArgGlnAlaIleThrAlaAlaIleLysAlaAlaValLysSerGlyIleLys
                                                                                                                                                          AATATTAAAAGAAATTCCGGAGTTACTGTTGAAAATTCTTTTGTGAAAAGCAGCTGAAAAA 8638
                                                                                                                                                                                                 ThrValAlaThrGlnIleThrValGlnAlaValValGlnAlaValLySGlnAlaValIle 327
                                                                                                                                                                                                                                                                                        AlaGlyAlaAlaValGlyAlaAlaAlaAlaGlyGlyAlaAlaGlyAlaAlaAlaAlaThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACAGCCGGTGGAGGAGCCGCAGGTCTTGCAGCAGTTACCGGAGTGGTTTCTGTTAACACT 8086
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -LysSerMetGluSerThrLeuGluSerLeuGlnSerLeuSerAlaAlaGln 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLO1840-ABLI6175) and the encoded proteins (ABB1737-ABB72072).
                                                                                                                                                                                                                                                                                                                                  3607
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P-PSDB; ABB59028.
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11-JUL-2000; 2000US-0614150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 3875; 21pp + Sequence Listing; English
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114 AlaThrLysIleAlaMetGlnThrSerIleGluGluAlaSerLysSerMetGluSerThr 133
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                                                GlnLysAlaGlyAlaAspThrGlyValSerGlyAlaAlaAlaThrThrAlaSerAsnThr 113
                                                                                                                      ThrLysThrGluThrAlaProGlnGlnGlyValAlaAlaGlyLysGluSerSerGluSer 93
                                                                                                                                                                                                                                      ThrLysGlnIleGlnGlnThrArgGlnGlyLysAsnThrGluMetGlu-------
                                                                                                                                                                                                                                                                       ACCACTGGCGTTATGACGCGATTGCAGCGCGAACAACAACAAAAGTCCGGCGGTCGTTCA 3726
                                                                                                                                                                                                                                                                                                                                  AGTTCGCGTAATCCAGCCAAGGCTCAGGCCGCACAGCCGCAGTGCATTATCGATTCGATG 3666
                                                                                                                                                                                                                                                                                                                                                            SerSerSerGlyProAspAsnGlnLysAsnIleMetSerGln---ValLeuThrSerThr
                               GCTGCAGCAGCGGCG-----
                                                                                          ACTAAGGCTGTCGAAGCA-----ACGGCTGCCGGTGAAAAGGTGGCCAAAGCG
                                                                                                                                                   AAAGCGGCAGCTGATGCTGCCAAAGCGGCTGAAAGTGCCGCCGAAAAGGCAAGCGCCGCC 3846
                                                                                                                                                                                                               TCCGCCGTTGCTGAGCGTGAGCGTGCGGAACGTGCCGCCGAGCGTGAGCGTGTGGCAGAG 3786
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                                ----GCGGCAGCAGCAACTACCGCCACAACCGCA 3939
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434	-SerGluMetGlnGlnAsnValAlaGlnPheGlnLysGluValGlyLysLe	418	Qy
4862	GCCGGGCAATTATCTTGGACAGAAGCTGAAGGCTGCCCAAGTTGAGGGTTTGGGAGCTGG	4803	ф
417	lAlaAlaProAlaLeuGlyLysGlyIleMetGlnMetGlnLeu	403	Qy
4802	GGCGGCGAATGAGAGTAGTAGTGGTGCCGGAGTGAATACCTATGGCCACACCGCAACAAC	4743	Db
403	uThrSerLysTrpValThrValGlyValGlyValValVa	390	Qy
4742	TGGCGATAAAATCGTCAAGACAACGCCATCATCCAGGGCGCCAAATTCTACATCTTCAAC	4683	Db
390	yThrGlnMetIleAlaLysAsnPheProLysLeuSerLysValIleSerSerLe	372	Qу
4682	GAACGCTGGTGGAGCAGCACCCGGATCGTTAGCAGCAACGAATGCATCGATTGCGACGAG	4623	Db
372	IleSerLysValPheAlaLysGl	365	Qy
4622	്റ <b>-</b>	4563	Db
364	· no	349	Qy
4562	AATGCAACGGGCGCC-TCTGCTCCAGTGCAGGGCGTTACCTTGAATGGCTTTAAGCCTGG	4504	Db
349	aI1	330	Qy
4503	AGGCTATCAATGCCGAGGGCTATAATGCTATCGGTGGCAACAGCAGCAGCAGCAGCAGC	4444	Дb
330	-Ala	311	Qy
4443	GCTGCTAAGGGAGCTGACTCTCGGCCAGATGCCAACGATCCGCTGGCCAAAACTGCTTCG	4384	Db
310	AlaAlaAlaThrThrValAla	304	Qy
4383	TGCCGCCAAGGGTGTTGGCAAACCGGAAACAGCGACTGAGCCAGCG	4324	Db
303	ValGlyAlaAlaAlaGlyGlyAlaAlaGlyAla	292	Qy
4323	AGTGCTGGCGAGGCGACAACGGCAACGGCCACGCCAC	4288	Db
291	IleValAlaAlaIlePheThrCysGlyAlaGlyLeuAlaGlyLeuAlaAlaGlyAlaAla	272	Qy
4287	ACGGTGGCCACTGCCGGTACACCGGCAACCGGAGCAAGTGCGGCC	4243	Db
271	– ĸ	252	Qу
4242	AGAGCAAAAATGCCGAGGAGGAGGCAGCTGCCACAGCCGGAGCAGCA	4195	Db
251	~ —	234	Qy
4194	CAACAGCACCACCAGAGATCTCAGCGGGCGGCGAG	4156	Db
233	AlaAspGlnThrAsnLysLeuGlyLeuGluLysGlnAlaIleLysIleAspLysGluArg	214	Qy
4155	GCAACAGCTGGTGGACCAACGGCAACGGGAACTCCGACAGCAGCAACTACACCTGCAACA	4096	Db
213	GlnThrLeuGlyGluAlaThrLysSerAlaLeuSerAsnTyrAlaSerThrGlnAlaGln	194	Qy
4095	AAGAATGCA	4087	Db
193	ProGlyValThrProArgSerGluValIleGluIleGlyLeuAlaLeuAlaLysAlaIle	174	Qy
4086	GATGCCGCCAAAACGGCTAGCGCCAGCGAT	4057	Db
173	SerGlySerAlaLysLeuGluThrProGluLeuProLys	154	Qy
4056	GCATCATCA TCGACGGCAAGTCCAGCGACATTGGCAGGAATAGCCGCAGATAAAACG	4000	Db
153	AlaAlaGlnMetLysGluValGluAlaValValVal	134	Qy
3999		3940	Db

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disorder e.g. arteriosclerosis, cancers; autoimmune/inflammatory disorder, AIDS, allergies, anaemia, asthma; cardiovascular disease e.g. congestive heart failure, ischaemic heart disease; developmental disorder e.g. renal tubular acidosis, hypothyroidism; neurological disorder e.g. Alzheimer's disease, dementia, Parkinson's disease, epilepsy or stroke. The SECP polynucleotide and polypeptide are further useful for analysing the proteome of a tissue or a cell type. The polynucleotide is useful for creating knockin humanised animals (pigs) or transgenic animals (mice or rats) to model human disease, and for somatic or germline gene therapy, and further for generating hybridisation probes useful in mapping the naturally occurring genomic sequence. This polynucleotide sequence represents the DNA of a human secreted protein of the invention.
  2068
                                                                                     2026
                                                                                                                                                                            1984
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 5; Page 218-220; 229pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human secreted proteins and polynucleotides for diagnosing, treating preventing disorders of cell proliferative, cardiovascular, developmental, neurological and autoimmune/inflammatory disorders -
                                                                                                                                                                                                                                                                                                                                                      1864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1753 -----AAGGACACCATCTACAGTGGGGTCACCAGTGCCGTGAACGTGGCCAAGGGG 1803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1714 ACAGGCATGGACACCACCAAAACT------GTCCTAACCGGTACC------ 1752
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6108 BP; 1313 A; 1838 C; 1971 G; 986 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated human secreted protein (SECP)
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                                                                                                                                                                                                                   106 AlaAlaThrThrAlaSerAsnThrAlaThrLysIleAlaMetGlnThrSerIleGluGlu 125
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                                    LysGluValGluAlaValValAlaAlaLeuSerGlyLysSerSerGlySerAlaLys 165
                                                                                     ACCAAGACTGTCCTAACTGGTACCAAGGACACCGTCTGCAGT
                                                                                                                                                                                                                                                                 ACAGCCAAGACCGTGCTGACCGGCACCAAGGACACAGTCACTACTGGGCCTCATGGGGGCA 1983
                                                                                                                                                                                                                                                                                                        AlaGlyLysGluSerSerGluSerGlnLysAlaGlyAlaAspThrGlyValSerGlyAla 105
                                                                                                                                                                                                                                                                                                                                                      GGCAGTGGGGTGACCGGTGCTGTGAATGTGGCCAAAGGGGCTGTCCAGACAGGTGTAGAC 1923
                                                                                                                                                                                                                                                                                                                                                                                             GlyLysAspLysThrSerSerThrThrLysThrGluThrAlaProGlnGlnGlyValAla 85
                                                                                                                                                                                                                                                                                                                                                                                                                                           GCTGTGCAAACTGGGCTGAAAAACGACCCAAAATATCGCGACAGGTACAAAGAACACCTTT 1863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SerGlyProAspAsnGlnLysAsnIleMetSerGlnValLeuThrSerThrProGlnGly 29
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                                                                                                                              AlaSerLysSerMetGluSerThrLeuGluSerLeuGlnSerLeuSerAlaAlaGlnMet 145
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-- GGGGTGACCGGTGCTGCGAATGTGGCCAAAGGGGCCGTCCAGACGGGT 2115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA, DNA or cDNA produced from an organism, amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification primers derived from the fragment of the S. pneumoniae genome to prime the amplification and isolating the amplified sequences. The computer readable medium can be used in a computer-based system for identifying fragments of the S. pneumoniae genome of commercial importance, or expression modulating fragments of the S. pneumoniae genome. Products from the present invention can be used in diagnosis kits and assays, ar pharmaceutical compositions and vaccines for S. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 isolated nucleic acid molecule encoding a homologue of any of the fragments of the S.pneumoniae genome (SEQ ID NO:1 to 391) where the nucleic acid molecule is produced by a process comprising; (a) screening a genomic DNA library using as a probe a target sequence defined by any of the sequences in SEQ ID NO:1 to 391, identifying members of the library which contain sequences that hybridise to the target sequence and isolating the nucleic acid molecules from the members; or (b) isolating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a computer readable medium which has the nucleotide sequences SEO ID NO:1 to 391 (AAV5214 to AAV52524) recorded on it, or a representative fragment or a sequence at least identical to SEO ID NO: 1 to 391. The nucleotide sequences depicted SEO ID NO: 1 to 391 to AAV52524) are genomic fragments from SEO ID NO: 1 to AAV52134 to AAV52524) are genomic fragments from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Computer-readable medium with recorded Streptococcus pneumoniae polynucleotide sequences - useful in diagnostic kits and assays, and pharmaceutical compositions and vaccines for Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus pneumoniae. The present invention also describes an
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  ThrLeuGlyGluAlaThrLysSerAlaLeuSerAsnTyrAlaSerThrGlnAlaGlnAla
                                                                                 GlyValThrProArgSerGluValIleGluIleGlyLeuAlaLeuAlaLysAlaIleGln
                                                                                                                                                                                                                                                 GluSerLeuGlnSerLeuSerAlaAlaGlnMetLysGluValGluAlaValValValAla
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                                                                                                                            TCTGAATCGGCATCAACGAGTGCGTCCGCTTCAGCAAGTACTAGC---
                                                                                                                                                                AlaLeuSerGlyLysSerSerGlySerAlaLysLeuGluThrProGluLeuProLysPro
                                                                                                                                                                                                         AGTACTAGCGCCTCAGCCTCAGCGTCAACAAGTGCATCGGCTTCAGCGTCAACGAGTGCG
                                                                                                                                                                                                                                                                                          TCAGCCTCAGCAAGTATCTCAGCGTCTGAATCGGCATCAACGAGTGCGTCCGCTTCAGCA
                                                                                                                                                                                                                                                                                                                              AlaMetGlnThrSerIle------GluGluAlaSerLysSerMetGluSerThrLeu
                                                                                                                                                                                                                                                                                                                                                                                                               AspThrGlyValSerGlyAlaAlaAlaThrThrAlaSerAsnThrAla - - - ThrLysIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCAGAGTCAGCAAGTACCAGTGCGTCAGCTTCCGCATCAACAAGTGCCTCGGCTTCAGCA
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                                                                                                            16-NOV-2000;
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                                         Yao MG,
                                                                      INCYTE GENOMICS
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Ding L, Lu DAM,

Sanjanwala M, Thornto Ding L, Hafalia AJA,

Tang , Lee

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Warren J, Lal Gietzen BΑ,

Honchell Tran B;

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                   AATGTGGCCAAGGGGGCCGTCCAGATG---
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            Choi GH,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTGCCTGGAAAATCCAAGAGCGGCTCGTCCAACAGCGGATCCGGCACAGGAGGAAGCTCG
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                                                                                                                                                                                                                                                                                                                                                                                    GlnAsnValAlaGlnPheGlnLysGluValGlyLysLeuGlnAlaAlaAlaAspMetIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ValValAlaAlaProAlaLeuGlyLysGlyIleMetGlnMetGlnLeuSerGluMetGln
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                                        AlaIleSerGlyAlaIleAlaGlyAlaHis
                                                                                   CCGCAGCT-AAAGAGACTTATGCAATGGCTTACGGAGAACCCCAATTACGAAGTGGATCC
                                                                                                                                                                        GAGGAGCCCGTACCAGTGATCAATAAACAGACAGGCAAACGCTTGGGAAGGCAATAAAGCG
                                                                                                                                                                                                                                                           CAGCAGCAGCAACAACAACAACACTCGATGCCCGGGCCACAGAATTTGACAGGA
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                                                                                                                                                                                                            -LysIleAlaSerLysGlnThrGlyGlu-----SerAsnGluMet 465
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                                                                                                                           AlaThrLysLeuGlyAlaGlnIleLeuLysAlaTyrAla 481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABA09498 standard; cDNA; 3750
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antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subjecg. arthritis and cancer – \,
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P-PSDB; ABB12254.
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27-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                homologue-encoding cDNA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                osteopathic; vasotropic; cardiant; virucide; antibacterial;
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2000US-0560875
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ΒP
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Claim 1; Page 968-969; 1963pp; English

cc sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and convention also relates to vectors and recombinant host cells comprising a nuclectide of the invention, methods of producing the novel polypeptides, and the polypeptides in a sample, and methods of identifying compounds which comprising a represent nucleic additions the novel polypeptides, corpolypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention although novel many of the corpolypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may differentiation activities; including cytokine, cell proliferation or cell differentiation activity; activin or inhibin-related activities; chaematopolesis regulatory activity; tissue growth activity; corpolated in oncogenesis, cancer cell proliferation or metastasis.

Cc involved in oncogenesis, cancer cell proliferation or metastasis.

Cc pepending on their biological activities, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoletic disorders (e.g., myeloid or lymphoid cell cancers, haematopoletic disorders (e.g., myeloid or lymphoid cell arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal

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RESULT 31
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The invention relates to an isolated nucleic acid detection reagent
                          Claim 1;
                                                            New isolated nucleic acid
genes from Drosophila and
                                                                                                    P-PSDB;
                                                                                                                                     Venter JC, Adams M,
                                                                                                                                                                                        23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                            23-MAR-2001; 2001WO-US09231
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                                                                                                                                                                                                                                                                                                     Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                              pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster expressed polynucleotide SEQ ID NO 14099
                                                                                                                                                                                                                                                                                                                                                                                           26-MAR-2002
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                                                  interactions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TrpValThrValGlyValGlyValValValAlaAlaProAlaLeuGlyLySGlyIleMet 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGCTCAGTGACTTCTAATTCATCAAAA----GAGAAGGTGTATTCTGCCTTACCTTCT---
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                                                                                                    ABB62436
                       SEQ ID NO 14099; 21pp + Sequence Listing; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -ACGGGTGACCAAGATTATTCTGTAACTGCTACTGCCTTAGGTTTAGGTTTAATG 2862
                                                                                                                                                                                                                                                                                                                           developmental biology;
cal; gene; ss.
                                                                                                                                                                                        2000US-191637P
2000US-0614150
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                                                             detection reagent for for elucidating cell s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence data for this patent did not form specification, but was obtained in electronic 1
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CAACATGCTTCACTCTCGCGACAATCATCTGGACAGTTCAGCAAGCCAGCTGTCCCCGCA 2887
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                                                                   ATGAAGACTCCTCCTCCCTCAATGGGTGCACCAATGGACCTTTCATCAAGCCTGCCGAAA
                                                                                                 LeuGluThrPro----
                                                                                                                                                                    ValValAlaAlaLeuSerGlyLysSerSerGlySer-----
                                                                                                                                                                                                                                                                                                                                           ATCGCCATTGACGTGGAGACGGAAAGGGCTAAGCTCCACGCTCTGCTTAACAGTTCTACA 270
                                                                                                                                                                                                                                                                                                                                                                                                                                              ValSerGlyAlaAlaThrThrAlaSerAsnThrAlaThrLys------ 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGTCACTGAGTGCAGCAACTGGCTCTTCG----
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                                   ProGlyValThrProArg
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                                                                                                                                                                                    27-OCT-2000;
24-NOV-2000;
07-MAR-2001;
                                                                                                                                                                                                                                                                                                          Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; gene; antiinflammatory; infection; vaccine; meningitis; gene therapy; ds.
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                                                                                                                                                                                                                                                                                        Streptococcus agalactiae.
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The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS
                                                  New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein \dot{}
                                                                                                                                                                                                                              29-OCT-2001; 2001WO-GB04789
                                Claim 7; Page 3556; 4525pp; English.
                                                                                           WPI; 2002-352536/38.
P-PSDB; ABP27418.
                                                                                                                           Tettelin
                                                                                                                                    Telford J,
                                                                                                                                                                  (CHIR-) CHIRON SPA.
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; 2000GB-0028727.
; 2001GB-0005640.
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CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in CC the specification. The proteins have antibacterial and antiinflammatory CC activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and CC antibodies that bind (I) are used in the manufacture of medicaments for CC the treatment or prevention of infection or disease caused by CC Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. CC Nucleic acids encoding (I) are used to detect Streptococcus in a CC biological sample. (I) is used to determine whether a compound binds to CC biological sample. (I) is used to determine whether a compound binds to CC used as a vaccine or diagnostic composition. The disease caused by CC used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be maningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity corrections.
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TyrGlnGluMetLysAlaAlaGluGlnLysSerLysAspLeuGluGlyThrMetAspThr 255
                                                                                                                                                     {\tt GlnThrAsnLysLeuGlyLeuGluLysGlnAlaIleLysIleAspLysGluArgGluGlu}
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                                                                                                                                                                                                                                                                                  US-09-889-314-2 (1-496) x AAD31881 (1-4645)
                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immune system modulation and treatment of autoimmune disorders and allergies; treatment of allergic responses to foods; reduction of blood lipids and prevention of heart disease; antihypertensive effect; prevention and treatment of urogenical infections, Helicobacter pylori, or hepatic encephalopathy; treatment of inflammatory bowel disorder and irritable bowel syndrome; modulation of endocarditis; and for improved protein and carbohydrate utilization and conversion. The transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    microbes in dairy manufacturing processes. The polynucleotides are useful for improving the properties of microbes used in the manufacture of milk-derived products such as cheeses, yogurt, fermented milk products, sour milks and buttermilk; in modifying the flavour, aroma, texture and health-related benefits of milk-derived products and in increasing the survival of microbes during industrial fermentation processes. The bacteria may be used to increase resistance to enteric pathogens and anti-infection activity, including treatment of rotavirus infection and infantile diarrhoea; aid in lactose digestion; as anti-cancer and anti-mutagenesis; liver cancer reduction; reduction of small bowel bacterial overgrowth; remune surface modulation.
                                                                                                                               2114 GAAGTTATTTCGAGTGCTGGATTCATTGTGAAAACAGCGACGGTAGTGATCAACGATGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 outer membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein and carbohydrate utilization and conversion. microbial population can be administered to a mammal carcinogenic agent. The present sequence is Lactobac:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to a new isolated polynucleotide comprising a sequence present in Lactobacillus rhamnosus strain HN001 and encoding a polypeptide capable of modifying the flavour, aroma, texture, nutritional and health benefits of milk-derived products, and/or survivability of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Fig 63; 257pp; English.
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28-NOV-2000;
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                                                     2174 GAAACGCCAAAGCAGGCATCCAGTGCAGCTGGCAGCTTAATCAACGCCAATAGTGCTGCT
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                                                                                                                                                                     21 GlnValLeuThrSer----
                                                                                                                                                                                                                                          1 AspThrAsnMetSerIleSerSerSerSerGlyProAspAsnGlnLysAsnIleMetSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polynucleotides and polypeptides from Lactobacillus rhamnosus, ful in e.g. improving the flavor, aroma, texture and health-related efits of milk-derived products, or in increasing properties of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2002-241760/29
               GlnIleGlnGlnThrArgGlnGlyLysAsnThrGluMetGluSerAspAla----
                                                                                     ---ThrProGlnGlyValProGlnGln-----AspLysLeuSerGlyAsnGluThrLys
                                                                                                                                                                                                         GACGGTAATTGGAGTTACGAACTGCCGACTGGGGTTTCGTTACCTGCCAATGCTTCATTT
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is Lactobacillus rhamnosus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GlyLeuGluLysGlnAlaIleLysIleAspLysGluArgGluGluTyrGlnGluMetLys 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GATTCCTACGCTTCTGAGGCCAGTGCCGCTTCTGCTGCTAATGATAGTTCGGGATATGCC 2593
                                                                                                                                                                                                 ArgGlnAlaIleThrAlaAlaIleLysAlaAlaValLysSerGlyIleLysAlaPheIle 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---MetAspThrValAsnThrValMetIleAlaValSerValAlaIleThrValIleSer 271
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                                                                  AACAGTAATGCGAGTGCCGCAGCCAGTGCGACCAAGGCTGGTGATAGCAAAGCCGCAGCA 3265
                                                                                                                                                                                                                                                                                                         GlnIleThrValGlnAlaValValGlnAlaValLys---GlnAlaValIleThrAlaVal 330
                                                                                                                                                                                                                                                                                                                                                                AGCGAGGCAGCAAAGGCA----AGCAGTAACGCGAGTGCCGCAACCAGCGCCGCG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACTGCATCATTTGCAGCAAGTTCCGCTGCGGCTGCCATGAGCGCAGCGTTATCGACAGCG 2653
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                                                                                                                  LysThrLeuValLysAlaIleAlaLysAlaIleSerLysGlyIleSerLysVal-----
                                                                                                                                                                   GAACAGGCGAAGACGGCTGCAAGTGCCGATGTGGTGGCAAGCAGTGCGGCCCAGCACGGCT 3205
                                                                                                                                                                                                                                                                                                                                                                                                       ValGlyAlaAlaAlaGlyGlyAlaAlaGlyAlaAlaAlaAlaThrThrValAlaThr 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IleValAlaAlaIlePheThrCysGlyAlaGlyLeuAlaGlyLeuAlaAlaGlyAlaAla 291
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                                                                                                                                                                                                                                                                 -GCCGTTGGTTTCAGTGCTGCCAGTGATGCAAGT 3145
--PheAlaLysGlyThrGlnMetIleAla 377
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FT / Parties XX	Ds	actobacillus rha ey L	<pre>KW anti-mutagenesis; immune system modulation; allerly; real concepts antihypertensive effect; urogenical infection; hepatic encephalopathy; KW bowel syndrome; endocarditis; transgenic microbe; outer membrane protein; KW rompA gene; ds.</pre>	XX  Enzyme; flavour; aroma; texture; nutritional; dairy manufacture; therapy;  KW fermentation process; anti-infection; rotavirus infection; heart disease;  KW infantile diarrhoea; lactose digestion; anti-cancer; autoimmune disorder;  KW infantile diarrhoea; lactose digestion; anti-cancer; autoimmune disorder;	AX DT 18-JUN-2002 (first entry) XX DE Lactobacillus rhamnosus outer membrane protein rompA gene.	AAD31881 ID AAD31881 standard; DNA; 4645 BP. XX XX AC AAD31881;	39 TGTC	Db 534379 GCGCGGCAGTCGGCAGATGGTGGGAGAAACCCTGTTGGACGGAC	534319 CCGTAGCAGCTGTGCATCGGCGGTAGCAAATAAAGGCAAATGTCGGGACGGCGCAATCG	534286 457	TACCGTACACGGAGAAGTAGCGA rMetPheThrGlnPheTrpGlnG	Db 534175 ATACCGCCATCAACGGCGGCAGCCTGAAAGACAACTTGGGCGGATGCCGCACTGGGTGCGA 534234  Oy 420 etG1nG1nAsnValAlaG1nPheG1nLysG1uValG1yLysLeuG1nAlaA 437  Oy 420 etG1nG1nAsnValAlaG1nPheG1nLysG1uValG1y	Db 534115 GTCCCGCAGCAGGCAAACTGACCGCTAACCTGATCAACAGCACCGCTGCCGCAAGTGTCC 5341/4  Oy 400 lyValValAlaAlaAroAlaLeuGlyLySGlyIleMetGlnMetGlnLeuSerGluM 420  iii		 533995 AACTG 362 erLys	Db 533935 CCAGCCAAGCCGCAGITICCCICATCATCATCATCATCATCATCATCATCATCATCATCATC		

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                                                                                                                                              sequences, which are all used in the exemplification of the present invention. The nucleic acid sequences, protein sequences, and antibodies against them, can be used in the manufacture of a composition. The composition can be used as a medicament (or in the manufacture of a medicament) for treating, preventing or diagnosing infection due to Neisserial bacteria. For example, some of the identified proteins could be components of vaccines against Meningococcus B; against all serotypes; and/or against all pathogenic Neissariae. Identification of sequences from the bacterium will also facilitate production of biological probes, particularly organism-specific probes. Attempts to make efficacious Meningococcus B vaccines have failed mainly due to antigen tolerance.
                                                  Multivalent vaccines have also been tried but none have successfully overcome antigenic variability. The provision of further, complete sequences may provide an opportunity to identify secreted or surface exposed proteins that may be presumed targets for the immune system a which are not antigenically variable or at least more conserved than
Sequence 1437668 BP;
                                                                                                                                                                                                                                                                                                                                                                Neisseria DNA sequences and their corresponding proteins; AAA81254 (AAA81259 and AAA81304 to AAA81321 represent PCR primers used in the isolation of Neisseria meningitidis DNA sequences; and AAA81322 to AAA81452 represent Neisseria meningitidis MenB polynucleotide ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes methods of obtaining immunogenic proteins from Neisseria genomic sequences. AAA81453 to AAA82414 represent specifically claimed Neisseria meningitidis genomic DNA sequences; AAA81260 to AAA81303 and AAB25620 to AAB25663 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 7; Page 866-1272; 1760pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated nucleotide sequences of Neisseria meningitidis which used in the diagnosis and treatment of N. meningitidis infectiother Neisserial infections, for example, N.gonorrhoea -
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Masignani V, Galeott
Rappuoli R, Pizza M;
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99US-0132068
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344338 A;
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C, Mora M,
353206 C;
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Ratti G, Scarselli
385074 G;
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355045 T; 5 other
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RESULT 27
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                              Pizza M,
Galeotti
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       Frazer CM,
                                                                                                                                                                                                                                                                                         30-APR-1999;
08-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                        08-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diagnosis; antigen; detection; infection; gene therapy; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neisseria meningitidis; Neisseria gonorrheae; immunogenic; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neisseria
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                                                                                                                                            (CHIR ) CHIRON CORP.
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Hickey E, |
C, Mora M,
M, Grandi G;
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                                      Peterson J, Ratti G, (
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Scarselli M,
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                                             Venter JC,
Scarlato V,
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                                         Masignani
Rappuoli F
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Claim 7;
                                                                                                                                                   WPI; 2000-647603/62
                                                                                                                                         Neisseria meningitidis B full length
                                                                                                                                     frames are used to detect, treat and
                                                                                                                           Appendix A; 692pp; English.
                                                                                                                                     genome sequence and open reading prevent Neisserial infections -
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The present invention describes the full length genome of Neisseria meningitidis B (NMB). The sequences in AAF21544 and AAF21607 CC Neisseria meningitidis B (NMB). The sequences in AAF21544 and AAF21607 CC to AAF21613 represent fragments of the NMB genomic sequence, as the CC sequence was too long to go in a record on its own it was split into 8 CC sequences which overlap each other at the beginning and end of each CC sequence by 49980 bp (i.e. the last 49980 bp of AAF21544 is repeated at CC the beginning of AAF21607, the last 49980 bp of AAF21547 are repeated at CC the beginning of AAF21608, and so on). AAF21545 to AAF21588 encode the CC expressor proteins given in AAB58550 to AAF21545 to AAF21589 to CC AAF21606 represent PCR primers which are used in the exemplification of the present invention. The NMB genome and fragments from it have CC expressor proteins and can be used in vaccines and gene therapy. CC expressor proteins and/or antibodies which binds to the CC proteins can be used in compositions for treating or preventing infection due to Neisserial bacteria or as a diagnostic reagent for detecting the bacteria. Computers, computer memory, computer storage medium or computer CC databases can be used in a search to identify open reading frames (ORFS) or coding sequences within the NMB genome. The DNA sequences provide further opportunities to find antigenic or immunogenic proteins which are more effective in vaccines than the outer membrane proteins which are

349980 BP; 84410 A; 84863 C; 94187 G; 86520 T; 0 other

US-09-889-314-2 (1-496) x AAF21607 (1-349980)	Alignment Scores: pred. No.: Score: Percent Similarity: Best Local Similarity: Query Match: DB:
x AAF21607	0.081 182.50 38.15% 22.78% 7.70%
(1-349980)	Length: Matches: Conservative: Mismatches: Indels: Gaps:
	349980 123 83 219 115

Qy Вþ Qy

	-688-60	-09-889-314-2 (1-496) x AAF21607 (1-349980)	
	17	AsnIleMetSerGlnValLeuThrSerThrProGlnGlyValProGlnGln 33	
•	233026	233026 AATCTGGTGGCAGCATCGACGCCTACGCCACCGCATTCGATGCCCCCAAAGGCAGCATTA 233085	85
-	34	AspLysLeuSerGlyAsn-GluThrLysGlnIleGlnGlnTh 47	
•	233086	233086 ACATCGAAGCCGGGCGGAAATTGACACTCTATGCCGTAGAAGAGCTCAACTACGACAAAC 233145	45
٠,	47	rArgGlnGlyLysAsnThrGluMetGluSerAspAlaThr-IleAlaGlyAlaSerGlyL 67	
•	233146	233146 TTGACAGCCAAAAAAGGCGCAGATTTCTCGGCATCAGCTACAGCAAAGCAC 233196	96
٠,	67	67 ysAspLysThrSerSerThrThrLysThrGluThrAlaProGlnGlnGlyValAlaAlaG 87	
•	233197	233197 ACGACACCACCCAAGTCATGAAAACCGCGCTGCCCTCAAGGGTAGTTGCA 233249	49
-	87	87 lyLysGluSerSerGluSerGlnLysAlaGlyAlaAspThrGlyValSerGlyAlaAlaA 107	
0	233250	GAATCTGCCAATCTGCAATCAGGTTGGGATACCAAACTGCAAGGCACACAGT 233	01
-	107	107 laThrThrAlaSerAsnThrAlaThrLysIleAlaMetGlnThrSerIleGluGluA 126	
0	233302	TTGAAACCACACTGGGTGGCGCAACCATACGCGCAGGCGTAGGCGAGCAGG 233352	52
_	126	126 laSerLysSerMetGluSerThrLeuGluSerLeuGlnSerLeuSerAlaAlaGlnM 145	
U	233353	CACGGGCCGATGCCAAGATTATCCTCGAAGGGATCAAAAGCAGCATCCACACAGAAACCG 233	12
~	145	145 etLysGluValGluAlaValValValAlaAlaLeuSerGlyLysSerSerGlySerAlaL 165	

멂 Qy B QΥ В QΥ 밁 δõ Вb Qy В

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RESULT 26
AAA81471/c
ID AAA81471 standard; DNA; 49914
                                              Alignment Scores: Pred. No.:
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    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                sequences, which are all used in the manufacture of a composition. The against them, can be used in the manufacture of a composition. The against them, can be used in the manufacture of a composition of a composition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes methods of obtaining immunogenic proteins from Neisseria genomic sequences. AAA81453 to AAA82414 represent specifically claimed Neisseria meningitidis genomic DNA sequences; AAA81260 to AAA81303 and AAB25620 to AAB25663 represent Neisseria DNA sequences and their corresponding proteins; AAA81254 AAA81259 and AAA81321 represent PCR primers used in the inclusion of Neisseria meningitidis DNA sequences; and AAA81322 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated nucleotide sequences of Neisseria meningitidis which can be used in the diagnosis and treatment of N. meningitidis infection and other Neisserial infections, for example, N.gonorrhoea -
                                                                                                             Sequence 49914
                                                                                                                                                                              sequences may provide an opportunity to identify secreted or surface exposed proteins that may be presumed targets for the immune system a which are not antigenically variable or at least more conserved than
                                                                                                                                                                                                                                        be components of vaccines against Meningococcus B; against all serotypes; and/or against all pathogenic Neissariae. Identification of sequences from the bacterium will also facilitate production of biological probes, particularly organism-specific probes. Attempts to make efficacious Meningococcus B vaccines have failed mainly due to antigen tolerance. Multivalent vaccines have also been tried but none have successfully overcome antigenic variability. The provision of further, complete
                                                                                                                                                                                                                                                                                                                                                                                               composition can be used as a medicament (or in the manufacture of a medicament) for treating, preventing or diagnosing infection due to medicament and treating preventing or diagnosing infection due to medicament for example, some of the identified proteins could be a second or treating the manufacture of the manufacture of a medicament of the manufacture of a medicament (or in the manufacture of a medicament) for treating the manufacture of a medicament (or in the manufacture of a medicament) for treating the manufacture of a medicament (or in the manufacture of a medicament) for treating preventing or diagnosing infection due to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAA81452 represent Neisseria meningitidis MenB polynucleotide ORF sequences, which are all used in the exemplification of the present invention. The nucleic acid sequences, protein sequences, and antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 7; Page 451-466; 1760pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Frazer CM, Hickey E,
Masignani V, Galeott
Rappuoli R, Pizza M;
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30-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neisseria meningitidis; Neisseria gonorrheae; genome; immunogenic; antigen; vaccine; diagnosis; infection; antibacterial; identification; meningococcus B; MenB; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N. meningitidis partial DNA sequence gnm_19 SEQ ID NO:19.
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                                                                                                                                                         more variable regions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                             ВP;
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99US-0132068
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  Conservative:
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Ratti G, Scarselli M,
                                                                                                             11423
                                                                                                             G; 13448 T;
                                                                                                                                                                              immune system and conserved than
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Qу	Qу	Qу	Qy Db	Db Qy	ОУ	Qy Db	Db Qy	Qу	Оy	Qу	Qу	Оy	Qy Db	Qу	Qу Db	Qy Db	US-0	Best L Query DB:
317	298 20509	278 20566	260 20626	240 20657	220 20702	200 20758	181 20809	165 20869	145 20929	126 20989	107 21040	87 21092	67 21145	47 21196	34 21256	17 21316	9-889-	: Local
lavalva   ::: CTATCAC	lyGly	hrCysGlyAlaGlyLeuAlaGlyLeuAlaAlaGlyAlaAlaValGlyAlaAlaAlaAlaGli	etIleAla ::::: TCGTTATC	ysAlaAl	euGlyLeuG	hrLysSerAlaLeuSerAsnTyrAlaSerThrGlnAlaGlnAlaAspGlnThrAsn 	luValIleGluIleGlyLeuAlaLeuAlaLysAlaIleGlnThrLeu :::::::::::    ACATTGTCGATAFTCCGAAAGGCAATCTGAAAACCCAAATCGAAACCCTC	ysLeuGluThrProGluLeuProLysProGlyValThrProArgSerG	etLysGluValGluAlaValValValAlaAlaLeuSerGlyLysSerSerGlySerAlaL ::::::::::::::::::::::::::::::::::::	laSerLy    CACGGGC	laThrTh    TTGAAAC	lyLysGl	ysaspLy     ACGACAC	rArgGlnGlyLysAsnThrGluMetG 	ACATCGA	AsnIleMetSerGlnValLeuThrSerThrProGlnGlyValProGlnGln	314-2 (	ocal Similarity Match:
.lGlnAlaVa     :CACAGCCGC	-AlaAlı       AGCAGC	yAlaGl:       ceceec	aValSerVa     CGTCGTAAC	aGluGl	uGluLy:	rAlaLe GCCCGA	eGluIl ::::   CGATAT	uThrPro :    ATTGCC	uValGlı ;; CAGCAA	erLysSerMetG : GGGCCGATGCCA	rAlaSe:       CACACTO	uSerSe:     -GAATC	SThrSe	GlyLysi      CCAAAA	ysLeuS     AGCCGG	etSerG ::::: TGGCAG	1-496)	rity:
1Lys AGG	aGlyAla      AGGAACO	yLeuAlaGlyL         AGGCGCAGGA-	rValAla AACCGT <i>I</i>	lnLysSer	sGlnAla GAATCAC	uSerAsr GTATGC1	eGlyLeı       rccgaa <i>ı</i>	oGluLet   GAGTTT(	uAlaVal :::: ATCTACI	tGluSer ::: CAAGATT	hrThrAlaSerAsnThrAlaThr            AAACCACACTGGGTGGCGCAACC	rGluSer   :::  rGCCAAT	rSerThr ; CCAAGTO	AsnThre : AAGGCGC	erGlyAs       GCGGAA	rGlnValLeuThrS ; AGCATCGACGCCTA	x AAA8147	22.78% 7.70% 21
sGlnAlaVal :::    CAAAGCCGC/	AlaAla         GCAGCC	aGlyLeu          GGA	alleThr :::    ATTGACC	LysAsp	IleLys :::::: GTGCAG	TYFAla      TATTTG	Ala	ProLys PACCGGT	ValVal ::: CTATGG	luSerThrLeuGluS :: AGATTATCCTCGAAG	AlaThr         GCAACC	GlnLys ::: CTGCAA	AspLysThrSerSerThrThrLysThrG 	lumetG ::::: :AGATT-	AspLysLeuSerGlyAsn-GluThr            :::    TCGAAGCCGGGCGGAAATTGACACT	uThrSe :: :GCCTAC	1471 (1	
CIC	yAlaalaGlyAlaAlaAlaAlaThTThrValAlaThrGln 	AlaAlaGlyAlaAlaValGl	tileAlavalServalAlaIleThrvalIleSerIleValAlaAlaIlePheT	SerLysAspLeuGluGlyThrMetAspThrValAsnThrValM        GAGGGCATGACACCCGCAGCAGCAGCTGTCG	luLysGlnAlaIleLysIleAspLysGluArgGluGluTyrGlnGluMe :::::::TGGAATCAGGTGCAGCTTGCTTACGATAATGGGACTACAAACAG	AlaLeuSerAsnTyrAlaSerThrGlnAlaGlnAlaAspGlnThrAsnLys	LeuAlaLysAlaIleGlnThrLeuGlyGluA     	LeuGluThrProGluLeuProLysProGlyVal- 	GluValGluAlaValValValAlaAlaLeuSerGlyLysSerSerGlySerAlaL ::::::     ::: AGCAGCAAATCTACTCTATGGCAAAAACAGGCAGGACGGGGCAGTAACATCGAAA	aSerLysSerMetGluSerThrLeuGluSerLeuGlnSerLeuSerAlaAlaGlnM 	ThrThrAlaSerAsnThrAlaThrLysIleAlaMetGlnThrSer	luSerSerGluSerGlnLysAlaGlyAlaAspThrGlyValS     :: :::::         :::GAATCTGCCAATCTGCAATCAGGTTGGGATACCAAACTGC	ThrGluT	ArgGlnGlyLysAsnThrGluMetGluSerAs             TGACAGCCAAAAAAGGCGCAGATT	-AspLysLeuSerGlyAsn-GluThrLysGlnIleGlnGlnTh 	rThrProG: :     :GCCACCGC	1-49914	Mism Inde Gaps
ThrAlaval; ;;;;; ;GCCAGTCTC	aThrThrValAl            AACCGGAGTAGC	lyAlaA         GAGCCG	VallleSerIleValAlaAlaI :::              GCACTGTCCGCCCCGGCAGCCG	lyThrM     GCATGA	ysglua: :::: ACGATA	Inalac	ysalai    CCCAAA	al	euSerG :::  AGGCAG	erLeuGln- ::::: GGATCAAAA	lametG: :::: ATAC	laaspTl       GGGATA	ThralaProGlnGlnGlyValal     :::        GCGCTGCCCTCAAGGGTAGTTGC	PAlaThr-IleAlaGly :::    ::: -TCTCGGCATCAGCTAC	CCGTAGA	GlnGlyValP :::  CATTCGATGC	_	Mismatches: Indels: Gaps:
alArgGl :: TC	laThrG     CAGCAG	laValG       CAGCAGO	erIleVa     CCGCCC	etAspTl CACCCG	rgGluG) ;; AATGGG!	lnalaas      TGCGA/	leGlnTl   :::   CGAAA	TACTGTC	lyLysSe   ::: GACGGG	SerLe    :  GCAGCAT	lnThrSe :: GCGCAG	hrGlyVa     CCAAACT	roGlnG]     CCTCAA	r-IleAl    :: GCATCAG	Lys AAGAGCT	ValProGI :::    ATGCCCC		: 219 115 24
lnAlaIl	lnIleThrVa ::: SCACATCAGO	lyAlaAlaAl          SAACGGCAGC	alAlaAl        :::    :::::::::::::::::::::::	hrValAs CAGCAGC	luTyrG1 ::   :: \CTACAA	spGlnTh \AAACAT	nrLeuGl	ThrPr	erSerGl     GCAGTAA	erLeuSerAlaAlaG   :::  GCATCCACACAGAAA	MetGlnThrSerIleGluG :::::      ATACGCGCAGGCGTAGGCGAGC	alSerGlyAla ::      GCAAGGCACA	LnGlyva ::    GGTAGT	IleAlaGlyAlaSerG    ::: :: ATCAGCTACAGCAAAG	GlnIle    :::  CAACTA	lnGln- ::: CAAAGG		- 55 60
eThrAl	1G1	aAlaAla       AGCCGG/	allePheT	GluGlyThrMetAspThrValAsnThrValM              GAGGGCATGACACCCGCAGCAGCTGTCG	nGluMet	Ly 	yGluAlaT    A	ThrProArgSei	ySerala CATCGA	aAlaGlı AGAAAC	-GluGluA    :::   CGAGCAGG	YAlaAlaA      CACACAGT	luThralaProGlnGlnGlyValAlaAlaG     ::        GCGCTGCCCTCAAGGGTAGTTGCA	AlaSerGlyL ;;; AGCAAAGCAC	LysGlnIleGlnGlnTh     :::::       GCTCAACTACGACAAAC	CAGCATTA		
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Chen Y,

Zychlinsky

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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cell, thereby producing the IpaB protein or derivative which in the cell, thereby producing the IpaB protein or derivative which induces apoptosis and kills the cell. This approach is useful in treating e.g. cancer, autoimmunity, inflammation and chronic viral creating e.g. and so be used to treat diseases that involve apoptotic concentanisms in their pathogenesis, e.g. AIDS, degenerative diseases conjury or toxin induced liver disease. Methods of gene therapy creating upon controlled expression of IpaB in a target cell are conference of interaction of an apoptosis inducing protein or peptide with ICE; conference of an apoptosis inducing protein or peptide with ICE; conference of an apoptosis inducing protein or peptide with ICE; conference of inhibiting the binding of IpaB to compound capable of inhibiting the binding of IpaB to compound capable of inhibiting the binding of IpaB to compound capable of inhibiting the binding of IpaB to compound capable of inhibiting the binding of IpaB to compound capable of inhibiting the binding of IpaB to compound capable of inhibiting the binding of IpaB to compound capable of inhibiting the binding of IpaB to compound capable of inhibiting the binding of IpaB to compound capable of inhibiting the binding of IpaB to compound capable of inhibiting the binding of IpaB to compound capable of inhibiting the binding of IpaB to compound capable of inhibiting the binding of IpaB to compound capable of inhibiting the binding of IpaB to compound capable of inhibiting the binding of IpaB to compound capable of inhibiting the binding of IpaB to compound capable of inhibiting the binding of IpaB to compound capable of inhibiting the binding of IpaB to compound capable of inhibiting the binding of IpaB to compound capable of inhibiting the binding of IpaB to compound capable of inhibiting 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence comprises DNA encoding the IpaB protein (see AAW29893) of Shigella flexneri. This protein induces apoptosis by binding to interleukin-1-beta converting enzyme (ICE). A claimed method of inducing apoptosis in a eukaryotic cell, thereby killing the cell, comprises: (a) providing to a cell to be killed a DNA molecule (I) in expressible form which encodes the Shigella IpaB protein or a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shigella IpaB protein induces apoptosis by binding to interleukin-1-beta-converting enzyme - useful for treating cancer, auto-immunity, inflammation, etc. by eradication of unwanted cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; Page 67-69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     316 AAGTCCCAGCAACAGGCAAGACAGCAAAAAAACCTAGAATTCTCCCGATAAAATTAACACT 375
                                                                                                                                                                                                                                                                                                                                                                                               436 AACGCAGATTCTAAAATAAAAGACCTAGAAAATAAAATTAACCAAATTCAAACAAGATTA 495
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136 SerLeuGlnSerLeuSerAlaAlaGlnMetLysGluValGluAlaValValValAlaAla 155
                                                                                                                                                                      532 TTAAGCCGGGAAGAA-----ATACAACTCACTATCAAAAAAAGACGCAGCAGTT 579
                                                                                                                                                                                                                                                                                   496 TCGAACCTCGATCCA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 56 GluSerAspAlaThrIleAlaGlyAlaSerGlyLysAspLysThrSerSerThrThrLys 75
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                                                                                                            LysIleAlaMetGlnThrSerIleGluGluAlaSerLysSerMetGluSerThrLeuGlu 135
                                                                                                                                                                                                                     AlaGlyAlaAspThrGlyValSerGlyAlaAlaAlaThrThrAlaSerAsnThrAlaThr 115
                                                                                                                                                                                                                                                                                                                                     ThrGluThrAlaProGlnGlnGlyValAlaAlaGlyLysGluSerSerGluSerGlnLys 95
                                                          AAW29893
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	475 GlnileLeuLysAlaTyrAlaAlaIleSerGlyAlaIleAlaGlyAla 490	Qу
1491	1432 GAAGTAATATCCAAACAAATTATTTCCACCCATTTAAACCAAGCAGTTTTATTAGGAGAA	DЬ
474	466ThrGlnLysAlaThrLysLeuGlyAla	Qy
1431	1372 GACGATTTAATCACTAATGCTGTTGCCAGATTAAATAAAT	Дb
465	452 SerLysIleAlaSerLysGlnThrGlyGluSerAsnGluMet	Qy
	1312 ATAGGTAAAACCCTCACAGACCTTATACCAAAGTTTCTCAAGAATTTTTCTCTCAACTG	Db
51	435GlnAlaAlaAlaAspMetIleSerMetPheThrGlnPheTrpGlnGlnAla	Qy
ı w	1273	Db
34	415 MetGlnLeuSerGluMetGlnGlnAsnValAlaGlnPheGlnLysGluValGlyLysLeu	Оу
1272	1231 GTCCTAGTTGCAGCAGTCGTTCTCGTAGCCACTGTTGGTAAA	Db
414	yIleMetG	Qy
1230	1171 GTCGACTCGAAAAAAGCCAAAATGATTGGCTCTATTCTGGGGGGCAATCGCAGGCGCTCTT	рb
394	375 MetIleAlaLysAsnPheProLysLeuSerLysValIleSerSerLeuThrSerLysTrp	Qy
1170	1126 AAACTCCTTTCAGATGCATTTACAAAAATGCTCGAAGGCTTGGGC	Db
374	355 LysalaileAlaLysAlaileSerLysGlyIleSerLysValPheAlaLysGlyThrGln	Qy
1125	AAT	Db
354	335 ThrAlaAlaIleLysAlaAlaValLysSerGlyIleLysAlaPheIleLysThrLeuVal	Qу
1065	1036 ACGGATGCTATAGTACAAGCAGCGACCGGC	Db
334	aValLysGlnAlaValIleThrAlaValArgGlnAlaI '	Qу
1035	1030ATGGTT	Db
314	1	Qy
1029	녆	Db
294	Ala	Qy
975		DЪ
274	lMetIleAlaValSerValAlaIleThrValIleSerIleValAla	Qy
924	AGAAGAACTCAACAGAGTAATGGGT	Db
254	yrGlnGluMetLysAlaAlaGluGlnLysSerLysAspLeuGluGlyThrMetAsp	Qy
876	GATGAG	Db
235	lnThrAsnLysLeuGlyLeuGluLysGlnAlaIleLysIleAspLysGluArgGluGlu	Qy
837	78 GTTGGAAAAATAATGAAGAATCTTTAAAAAATGATCTGGCTCTATTCCAGTCTCTCAA	Db
215	qs	Qy
777	ATGGCAACCTTTATTCAACTA	Db
195	6 ValThrProArgSerGluValIleGluIleGlyLeuAlaLeuAlaLysAlaIleGlnThr	Qy
735	679 TTTTCAAACACAGCATCTGCTGAACAGCTATCAACCCAGCAGAAAATCATTAACCGGA	Db
175	56 LeuSerGlyLysSerSerGlySerAlaLysLeuGluThrProGluLeuProLysProGly	Qy
678		Db

301	laAlaAlaAlaGlyGlyAlaAla	Qy 290 AlaAlaValGlyA 	n
891	dalalieprefricysclyalactyleualactyleualactyleualacts 	CY 2/1 SETITEVALATAR ::: Db 832 GCTAAGGATGGAA	
w	CAGATTGCTGCTGCTATTGCTTTGAGGGGGGAT	799	
270	hrValAsnThrValMetIleAlaValSerValAlaIleThrVal	Qy 251 GlyThrMetAspT	0
250 798	luGluTyrGlnGluMetLysAlaAlaGluGlnLysSerLysAspLeuGlu 	Qy 232GluargGluG :::     Db 745 GGTGATGCGGAGA	п О
744	AAAGAAGCCTGGGGATGCTAAAAATCCGATTGCTGCTGCTATTGGGAAG	85 GATCAGGAGGG	
231	tysLeuGlyLeuGluLysGlnAlaIleLysIleAsp	Qy 214 AlaAspGlnThrAsn	0
213 684	/GluAlaThrLysSerAlaLeuSerAsnTyrAlaSerThrGlnAlaGln 	Oy 195 ThrLeuGlyG :::      Db 625 GCTGTTAGTGGGG	
624		- 60	_
194	SerGluValIleGluIleGlyLeuAlaLeuAlaLysAla	Qy 175 GlyvalThrProArg	0
	CAGTGAGGCTGCTAGCAAG	74 GCTCATGCTGGG	- 4
174		155 Alato	, r
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n F		יייייייייייייייייייייייייייייייייייייי	, ,
141	SerMetGluSerThrLeuGluSerLeuGlnSerLeuSer  SerMetGluSerThrLeuGluSerLeuGlnSerLeuSer   : : : : : : : : : : : : : : : : : : :	Qy 125 GluAlaSerLyss	- O
453	TGGCTGATGATAATGCTGCAAGGTTGCTGATAAGGCGAGTGTGAAG	Db 394 ATTGGAGAAGTTGTGGC	п
124	\SerAsnThrAlaThrLysIleAlaMetGlnThrSerIle	Qy 105 AlaAlaAlaThrT	0
393	AAAAGCTGTAAAGACAGCTGAGGGGG	Db 334 TTGGATAAGCTGGT	П
104	AlaGlyAlaAspThrGlyValSe	Qy 90 SerSerGluSerG	0
333	The Control of the	OY // SETTRITITLYSTRIGE :::	
	CTGCTGCTATTGCTTTGAGGGGGGATGGCTAAGGATGGAAAGT	ZI4 AAGGATGATCAG	, ,
1 1-4	laGlyAlaSerGlyLysAspLysThrSe	57 SerAspAlaThr	
		154 ATTGCTGCTGC	ь .
ת	vI.vsAsnThr:	Ov 45 GlaGlaThrArac	2
153		::: 100 GCTGCT	0
	yValProGlnGlnAspLysLeuSerGlyAsnGluThrLysGlnIl	25 SerThrProGln	o.
24 99	erSerGlyProAspAsnGlnLysAsnIleMetSerGlnValLeuThr 	Qy 5 SerIleSerSerS :::::   ::: Db 52 GCTGTTAGTGCTG	o 0
	x AAT85043 (1-7766)	US-09-889-314-2 (1-496)	c
	37.00% Conservative: 76 23.29% Mismatches: 223 7.85% Indels: 126 18 Gaps: 25	Percent Similarity: Best Local Similarity: Query Match: DB:	CO m m

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                                                                                                                                                                                                                                                       IpaB; apoptosis; interleukin-1-beta converting enzyme; ICE; cacner;
autoimmune disease; inflammation; AIDS; degenerative disease;
Alzheimer's disease; myelodysplastic disorder; ischaemic injury;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1177
                                                                                                                                                                                                 Shigella flexneri
                                                                                                                                                                                                                                                                                                                                Shigella flexneri IpaB gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1444 GGTGAGAAAGGGAAG---GCTGAGGGGGGCTATTAAGGGAGCTGCTGAGTTGTTGGATAAG 1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1390 GCTATTGCTTTG-----AGGGGGGATGGCTAAGGATGGAAAGTTTGCTGTGAAGGATGGT 1443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1072 GCTGGGGGGAGTGAA----
                                                    25-JAN-1996;
                                                                                      10-JAN-1997;
                                                                                                                           31-JUL-1997
                                                                                                                                                            WO9726790-A1
                                                                                                                                                                                                                                     toxin-induced liver disease; gene therapy; shigellosis; ss.
                                                                                                                                                                                                                                                                                                                                                                     10-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                         AAT85939;
                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT85939 standard; DNA; 1743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1294 GCTACAAATCCGATTGCTGCTGCTATTGGGAAGGGT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1012 GTTGCTGATAAGGCGAGTGTGACGGGGATTGCTAAGGGGGATAAAGGAGATTGTTGAAGCT 1071
               (UYNY ) UNIV NEW YORK STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             892 GCTATTAAGGGAGCTGCTGAGTTGTTGGATAAGCTGGTAAAAGCTGTAAAGACAGCTGAG 951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGGCTTCAAGTGGTACTGATGCAATTGGAGAAGTTGTGGCTAATGCTGGTGCTGCAAAG 1011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGGTAAAAGCTGTAAAGACAGCTGAGGGGGGCTTCAAGTGGT 1542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MetIleSerMetPheThrGlnPheTrpGlnGlnAlaSerLysIleAlaSerLysGlnThr 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MetGlnGlnAsnValAlaGlnPheGlnLysGluValGlyLysLeuGlnAlaAlaAlaAsp 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ValGlyValGlyValValValAla------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGTGAGGCTGCTAGCAAGGCGGCTGGTGCTGTTAGTGCTGTTAGTGGGGAGCAGATATTA 1236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AlaValLysGlnAlaValIleThrAlaValArgGlnAlaIleThrAlaAlaIleLysAla 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GlyAlaAlaAlaThrThrValAlaThrGlnIleThrValGlnAla---ValValGln 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GlyGluSerAsnGluMetThrGlnLysAlaThrLysLeuGlyAlaGlnIleLeu-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGTAATAAAGGGGCAGGGAAGTTGTTTGGGAAGGCTGGTGCTGGTGCTAATGCTGGGGAC 1176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----LysalaTyrAlaAlaIleSerGlyAlaIleAlaGly 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AATGAGGAGAATGGTGCGGAGTTTAAGGATGAGATGAAGAAGGATGATCAGATTGCTGCT 1389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGTGCGATT---GTTAAGGCTGCTGATGCGGCTGATCAGGAGGGAAAGAAGCCCTGGGGAT 1293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PheProLysLeuSerLys-----ValIleSerSerLeuThrSerLysTrpValThr 396
                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                  96US-0591079
                                                                                      97WO-US00399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----AAGCTGAAAGTTGCTGCTACAGGGGAG 1116
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7696 GGCAAAACAAATGTTGGCAAAAAGAAAGCTGCAACGCCA---GCAGCAGCAGCAGCAGCA
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                                                                                                                                                                                                                                                                                                                                                Variable major protein-like sequence; VMP-like sequence; vls locus; vlsE gene; Lyme disease; relapsing fever; therapy; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAT85043 standard;
                                                                                                                                                                                                                                                                                                        Borrelia burgdorferi strain B31-5A3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCAGCAGCCGCCGCACCAGCAGCAGCAACAGCAACAGAAGCTGTT---ACGGCTTTGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAGAGCAATGTGACCCCAATCAATGCCGATCAATTTATAACGCTGGCCCCCACAAAGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AsnTyrAlaSerThrGlnAlaGlnAlaAspGlnThrAsnLysLeuGlyLeuGluLys---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               {\tt AspThrValAsnThrValMetIleAlaValSerValAlaIleThrValIleSerIleVal}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCCAAAACATCACCGAACAAGCAGCAAGCATTGCAATTGCAACAGCAACACGAGGAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCACAACGCCCACAACA---ATAACAATTGGTGTTGCTGCTGTTAATGTTGCTGCTGTT 7346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAGCGGCAGCAGCAACAGGCCACAAATGCGTCATCGCCGGCGGCAACTGGCGATGCA 7403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----TyrGlnGluMetLysAlaAlaGluGlnLysSerLysAspLeuGluGlyThrMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AlaAlaAlaAlaGlyGlyAlaAlaGlyAlaAlaAlaAlaThrThrValAlaThrGlnIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCTGTTGTTGCTTCTGCTGCTGCTGCTGCTACTGATGCTGCTGCTGATGCGACTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AlaAlaIlePheThrCysGlyAlaGlyLeuAlaGlyLeuAlaAlaGlyAlaAlaValGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACAGTATCGAATTTGGCACAGTGTCTGCGA 7196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCGCTCAGCAGCAACAACAGCTGCGGCGAAGGCGTCGGCAATAATTTATCAAAGTTTGCA 7226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ThrValGlnAlaValValGlnAlaValLys
                                                                                                                                                                                                                                                                                                                                                                                          variable major protein (VMP)-like sequence (vls) locus.
                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                /label= vis6
3010..3482
                                                                                                                       /label= vls3
1870..2420
/*tag= f
/label= vls7
3484..3990
                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                   2440
                                                                                                                                                                                                                          /*tag= a
/label= vls2
/note= "truncated
                                                                                             /*tag= d
/label= vls5
                                                                                                                                                                                                              12..1293
                                                                                                                                                                     294..1869
                                                                                                                                                                                  *tag= b
label= vls3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA;
                                                                                   ..3009
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                                                                 Pred. No.:
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                                                                                         which consists of 15 silent vls cassettes (vls2-vls16) and an expressed vlsE gene (see AAT85043). Portions of several of the 15 silent vls cassette sequences, located approx. 500 bp upstream of vlsE, recombine into the central vlsE cassette region during infection, resulting in antigenic variation of the expressed lipoprotein (see AAW22676) and hence immune evasion, long-term survival and pathogenesis in the mammalian host. Nucleic acids, survival and pathogenesis, encoding VMP-like proteins, can be including vls2-vls16 sequences, encoding VMP-like proteins, can be used for the recombinant production of VMP-like proteins, or for the diagnosis of Lyme disease (claimed), and may also have application in DNA vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-AUG-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9731123-A1
                                                                                                                                                                                                                                                 This DNA sequence comprises the variable major protein (VMP)-like sequence (vls) locus of Borrelia burgdorferi. An infectivity related 28-kb linear plasmid, pBB28La, of B. burgdorferi B31 was isolated by subtractive hydridisation. It contained the vls locus,
                                                                                                                                                                                                                                                                                                                                                 Nucleic acid encoding variable major protein-like
Borrelia - useful for recombinant production of v
peptide, or for diagnosis of Lyme disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TEXA ) UNIV TEXAS SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-FEB-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Barbour AG,
                                                                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                        26; Page 101-105; 130pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hardham JM,
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/label= vls8
3991.4548
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/label= vls15
/note= "the vls sequence provided
/note= 7766 bases"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= m
/label= vls14
7274..7946
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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genes from Drosophila and
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIGHT6-ABLIGHT7), expressed DNA sequences (ABLIGHT8-ABLIGHT9) and the encoded proteins (ABB7737-ABB72072).
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pharmaceutical; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511) and the encoded proteins
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                                                                                                                                                                                                                                                                                                        specification, but was obtained in electroni
at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                     The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                sequences (ABL01840 (ABB57737-ABB72072)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-MAR-2002
                                                                                                                                                                                                                                      No.:
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GluMetGluSerAspAlaThrIleAlaGlyAlaSerGlyLysAspLysThrSerSerThr 73
                           CCAGCAGCACCAAAGACAATGGCCAAGATCAGCATGACAACAATGGCAGGAACAACT
                                                                                 ACAACACCACAAAAAACACCACAAGTT---AAGGCAGCAACAGATGAGTCCAAGTCAACA
                                                                                                           SerThrProGlnGlyValProGlnGlnAspLysLeuSerGlyAsnGluThrLys-----
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2000US-0614150.
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                                                                                                                                                                                                                                                                               BP; 1594 A; 1190 C; 1087 G; 767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene;
                                                                                                                                                                0.000244
186.50
38.00%
22.86%
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                                                    -GlnIleGlnGlnThrArgGlnGlyLysAsnThr 53
                                                                                                                                                                Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Human; dentin sialophosphoprotein precursor; dentin sialophosphoprotein; DSPP; dentinogenesis imperfecta type II; deafness; auditory; chromosome 4q21; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                    exon
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30-AUG-2001; 2001WO-CN01292.
                                               polyA_signal
                                                              polyA_signal
                                                                                   misc_feature
                                                                                                                                                  intron
              01-AUG-2002.
                            WO200258722-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dentin sialophosphoprotein precursor (DSPP) gene SEQ ID NO:1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                            2387..2431
/*tag= f
2432..7893
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/product= "dentin sialophosphoprotein"
/note= "contains introns"
2432..5520
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/number= 1
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/*tag= n

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5521..7893

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/note= "contains introns"
                                                                                    /product= "
5596..5604
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/number= 4
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/number= 3
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/note= "contains introns"
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8171..8176
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/note= "cell binding domain"
7988..7993
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                                                                                                                                                                                             8661..3793
                                                                                                                                                         'number= 4
                                                                                                                                                                                                                                *tag=
                                                                                                                                                                                                                  ..3660
                                                                                           "phosphophoryn"
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3-09-889-314-2 (1-496) x ABQ73537 (1-8201)

Matches: Conservative: Mismatches: Indels: Gaps:

Percent Similarity:
Best Local Similarity:
Query Match:

0.00044 187.00 39.24% 21.12% 7.89%

8201 106 91 251 56

Alignment Scores:

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Score:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mediated immune response involves providing a reservoir or other supply in the subject's body so that a SIBLINGS protein can be dispersed to interfere with complement mediated lysis and inflammation. This protects cells that are grafted onto foreign tissue or bone marrow cells introduced into a foreign host. The SIBLINGS protein can be BSP, OPN, DMP1 or DSPP. A method of detecting a SIBLINGS protein in a sample from a subject suspected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is that of DNA encoding human dentin sialophosphoprotein (DSPP, see AAB19772), a member of the small integrin binding ligand, N-linked 91ycoproteins (SIBLINGS) family. The invention provides methods and compositions for exploiting the discovery that members of the SIBLINGS family bind to complement Factor H, conferring resistance to complement mediated lysis. A claimed method of conferring protection against a complement
                                                            6814
                                                                                                                                                                                                                 6694
                                                                                                                                                                                                                                                                                                                                                                    6574 GACAGCAGTGATAGCGACAGCAGCAATAGCAGTGACAGCAGTAATAGTAGTGACAGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                   6514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6394 GACAGTAGCGATAGCAGTGACAGCAGCAGCAGTGACAGCAGTGATAGCAGTGACAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Detecting small integrin-binding ligand N-linked glycoproteins for detection of a tumor or protection against a complement mediated immune response, comprises detection where Factor H is not an inhibitor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-679515/66.
P-PSDB; AAB19772.
                                                                                                                                                                                                                                                                                            6634 GATAGCAGCAACAGCAGTGATAGCAGCAGCAGCAGCAGTAGCAGTGACAGCAGTGATAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       No . .
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                                                                                                                                                                                                                                                                                                                                                                                                        61 IleAla------GlyAlaSerGlyLysAspLysThr 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 GlnValLeuThrSerThrProGlnGlyValProGlnGlnAspLysLeuSerGlyAsnGlu 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AspThrAsnMetSerIleSerSerSerSerGlyProAspAsnGlnLysAsnIleMetSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      having abnormal bone turnover, especially osteoporosis, is also
aValValAla---AlaLeuSerGlyLysSerSerGlySerAlaLysLeuGlu-----
                                                                                                                                                                                                                                                                                                                          SerSerThrThrLysThrGluThrAlaProGlnGlnGlyValAlaAlaGlyLysGluSer 90
                                                            GACAGCAGCAATAGAAGTGACAGTAGTAATAGTAGTGACAGCAGCGATAGCAGTGACAGC
                                                                                            tGluSerThrLeuGluSerLeuGlnSerLeuSerAlaAlaGlnMetLysGluValGluAl 150
                                                                                                                                                                       aSerAsnThrAlaThrLysIleAlaMetGlnThrSerIleGluGluAlaSerLysSerMe 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGCAGTGATAGCAGCAACAGCAGTGATAGCAGCAACAGCAGTGATAGCAGTAGCAGT
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                                                                                                                                    AGCAACAGCAGTGACAGCAGTGATAGTGACAGCAGCAGCAACGAAAGCAGCAAT
                                                                                                                                                                                                                                                 SerGluSerGlnLysAlaGlyAlaAspThrGly-ValSerGlyAlaAlaAlaThrThrAl 110
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187.00
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21.12%
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ŏ	6859	AGTGATAGCAGCAACAGCAGTGACAGCAGTGATAGCAGCAACAGCAGTGATAGCAGTGAA 6918
¥	168	ThrProGluLeuProLysProGlyValThrProArgSerGluVa 182
ਰ	6919	AGCAGTAATAGTAGTGACAACAGCAATAGCAGTGACAGCAGCAGCAGCAGTGACAGCAGT 6978
¥	182	lileGluIleGlyLeuAlaLeuAlaLysAlaIleGlnThrLeuGlyGluAlaThrLysSe 202
ŏ	6979	CAGTGACAGCAGTAATAGTAGTGACAGC-AGCAATAGCGGTGACAGCAAC
Y Y	202	rAlaLeuSerAsnTyrAlaSerThrGlnAlaGlnAlaAspGlnThrAsnLysLeuGlyLe 222
: (	333	
ਲੋਂ ਵੇ	7098	CAGTGACAGCAGTGATAGCAGTGACAGCAGTGACAGCAGTGATAGCAGCAGCAACAGCAGTGA 7157
₹	242	GluGlnLysSerLysAspLeuGluGlyThrMetAspThr-ValAsn 2
ŏ ·	7158	AGCAGTGACAGCAGTGACAGCAGTGATAGCAGTAATAGTGACAGCAGCAACAGCAG 7
÷ ₹	258	ThrValMetIleAlaValSerValAlalleThrValIleSer::leValAlaAlalle- 276
	) 1	
ਝੋਂ ਝੋਂ	7278	
Ϋ́	293	lyalaalaalaalaGlyGlyalaalaGlyalaalaalaalathrThrValalaThrGlnI 313
ਲੋ	7338	CAGCAGTGATAGCAGTGACAGCAGTGATAGCAGCGATAGCAGTGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCA
Ϋ́	313	alGlnAl
ŏ	7398	TGACAGCAGTGACAGCAGTGAAAGCAGCGACAGCGATAGCAGCGACAG 7448
÷ ×	333	lalleThrAlaAlalleLysAlaAlaValLysSerGlyIleLysAlaPheIleLysThrL 353
ŧ		
ĕ ₹	353 7503	euVallysAlaileAlaLysAlaileSerLysGlyIleSerLysValPheAlaLysGlyT 373 euVallysAlaileAlaLysGlyT 373 euVallysAlaileAlail
γ	373	ysAsnPheProLysLeuSerLysVa
ŏ	7545	CAGCAGTGATAGCAGTGACAGCAGCGACAGCAG 7577
ìУ	393	ysTrpValThrValGlyValGlyValValValAlaAlaProAlaLeuGlyLysGlyIleM 413
ъ	7578	CGATAGCAGCGACAGCAGTGATAGTGATAGCAGTGACAGCAGTGACAGCAGCGACAG 7637
у	413	etGlnMetGlnLeuSerGluMetGlnGlnAsnValAlaGlnPheGlnLysGluValGlyL 433
ъ	7638	CAGTGACAGCAGCAGCAGTGACAGCAGCGACAGCAGTGACAGCAATGAAAGCAGCGA 7697
γ	433	~
й	7698	CAGCAGTGACAGCGATAGCAGTGACAGCAGCAGCAGTGAC-AGCAGCGACAGCA 7756
Ŋ	453	SerLysGlnThrGlyGluSerAsnGluMetThrGlnLysAlaT
ğ	7757	GACAGC
γ	473	ly 473
Ъ	7817	GT 7818

RESULT 20 ABQ73537

IJ

ABQ73537 standard; DNA; 8201 BP

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Alignment Scores:
Pred. No.:
Score:
Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expression modulating fragments of the S. pneumoniae genome. Products from the present invention can be used in diagnosis kits and assays, pharmaceutical compositions and vaccines for S. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1436 BP; 357 A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACAAGTGCGTCGGCTTCAGCAAGTACCTCAGCGTCTGAATCAGCATCAACGAGTGCATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  {\tt ThrAsnMetSerIleSerSerSerSerGlyProAspAsnGlnLysAsnIleMetSerGln}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCTTCGGCCTTCAGCGTCAACGAGTGCGTCTGAGTCAGCCATCAACGAGTACGTCAGCCTCA
                                                                                                                                                                                                                                GCTTCAGCAAGTACCAGTGCGTCAGCCTCAGCGTCGACA----AGTGCGTCGGCTTCA
                                                                                                                                                                                                                                                                                                                                                     ValValAlaAlaLeuSerGlyLysSerSerGlySerAlaLysLeuGluThrProGluLeu
                                                                                                                                                                                                                                                                                                                                                                                                                   GCCTCAGCAAGTACTAGCGCCTCAGCCTCAGCATCAACGAGTGCGTCCGCTTCAGCAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SerThrLeuGluSerLeuGlnSerLeuSerAlaAlaGlnMetLysGluValGluAlaVal 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----ThrLysIleAlaMetGlnThrSerIle---GluGluAlaSerLysSerMetGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCCTCAGCTTCAGCAAGTACCAGTGCGTCAGCCTCAGCAAGTACCAGTGCTTCAGCCTCA
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  IleAspLysGluArgGluGluTyrGlnGluMetLysAlaAlaGluGlnLysSerLysAsp
                                                                                        AlaGlnAlaAspGlnThrAsnLysLeuGlyLeuGlu-----LysGlnAlaIleLys
                                                                                                                                     GCAAGTACCTCAGCGTCTGAATCAGCATCAACAAGTGCGTCGGCTTCAGCATCAACGAGT
                                                                                                                                                                                AlaIleGlnThrLeuGlyGluAlaThrLysSerAlaLeuSerAsnTyrAlaSerThrGln
                                                                                                                                                                                                                                                                           ProLysProGlyValThrProArgSerGluValIleGluIleGlyLeuAlaLeuAlaLys
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                                                                                                                                                                                                                                                                                                      CCAGCCAAGCCGCAGTTTCCCTCATCAACAACAAAGGAGACATAAACCATACCCTGAAAG
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Streptococcus pneumoniae. The present invention also describes an isolated nucleic acid molecule encoding a homologue of any of the fragments of the S.pneumoniae genome (SEQ ID NO:1 to 391) where the nucleic acid molecule is produced by a process comprising: (a) screening a genomic DNA library using as a probe a target sequence defined by any of the sequences in SEQ ID NO:1 to 391, identifying members of the
                                                                                      The present invention describes a computer readable medium which has the nucleotide sequences SEQ ID NO:1 to 391 (AAV5214 to AAV52524) recorded on it, or a representative fragment or a sequence at least identical to SEQ ID NO: 1 to 391. The nucleotide sequences depicted SEQ ID NO:1 to 391 (AAV52334 to AAV52524) are genomic fragments from
                                                                                                                                                                                                                        Computer-readable medium with recorded Streptococcus pneumoniae polynucleotide sequences - useful in diagnostic kits and assays, pharmaceutical compositions and vaccines for Streptococcus
                                                                                                                                                                               Claim 1;
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                                                                                                                                                                                                                                                           N. gonorrheae; N. lactamica; chromosome Z2491; region 1; region 3; pathogenicity; blood-brain barrier; diagnosis;
                                                                                                                                                                                                                                                                                               DNA sequence that
                                                                                                                                                                                                                                                                                                                     22-OCT-1998
                                                                                                                                                                                                                                                                                                                                            AAV03553;
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                                                                                                                                                                                                                           meningitidis
                                                                                                                                                                                                                                                                                                                    (first entry)
         /note= "encodes AAW42637"
12794..13066
                             /*tag=
                                              /note= "encodes
12118..12609
                                                                              /note- "encodes AAW42635"
10127..12121
                                                                                                                  9044..9475
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                                                                                                                                                                                                                                                                                             is specific
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                                                         AAW42636
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47

Percent Similarity:
Best Local Similarity:
Query Match:

0.000437 191.50 38.33% 22.96% 8.08%

Matches: Conservative: Mismatches: Indels:

83 218 115 24

15620 124

US-09-889-314-2 (1-496) x AAV03553 (1-15620)

19

17

34

---AspLysLeuSerGlyAsn-GluThr-----

9936 AATCTGGTGGCAGCATCGACGCCTACGCCACCGCATTCGATGCCCCCAAAGGCAGCATTA 9995

ACATCGAAGCCGGGCGGAAATTGACACTCTATGCCGTAGAAGAGCTCAACTACGACAAAC

---LysGlnIleGlnGlnTh

47 10055

67

AsnIleMetSerGlnValLeuThrSerThrProGlnGlyValProGlnGln-----

Alignment Scores:

Pred

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Vinals C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genes present in Neisseria meningitidis but not other Neisseria species - and related host cells, RNA, anti-sense sequences, polypeptide(s) and antibodies, useful for diagnosing Neisseria meningitidis infection and in protective vaccines
                                             sequences common to N. meningitidis and N. gonorrheae, but absent from N. lactamica, are responsible for colonisation and penetration of the mucosa. The DNA sequences can be used to produce probes and primers, a antibodies produced against the encoded proteins are used in standard hybridisation/immunoassay processes for diagnosis of N. meningitidis infection, particularly meningitis.
                                                                                                                                                                                                                                                                                                                                                                                                AAV03518-53 represent sequences that are present in Neisseria meningitidis but not in N. gonorrheae or N. lactamica, except for the genes involved in biosynthesis of the capsule polysaccharide, frpA or C. opc, porA, rotamase, sequence IC1106, IgA protease, pillin, pilC, proteins which bind transferrin and opacity proteins. The sequences are proteins which bind transferrin and opacity proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-110594/10.
P-PSDB; AAW42633, AAW42634,
AAW42639; P-PSDB; AAW42640,
                                                                                                                                                                                                                                         found on chromosome 22491, mainly (or within 20 kb) between tufA and pilT (region 1), pilO and lambda 740 (region 2) or argf and opaB (region 3). The DNA sequences are responsible for the differences in pathogenicity between N. meningitidis and N. gonorrheae, specifically they include the genes that allow N. meningitidis to cross the blood-brain barrier. DNA genes that allow N. meningitidis to cross the blood-brain barrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 8; Pages 67-78; 150pp; French.
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Sequence 15620 BP;
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14241..15176
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13297..14238
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   4806 A; 3505
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         3556 G; 3753 T; 0 other;
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  Query Match:
                         Best Local Similarity:
                                            Percent Similarity:
                                                                 Score:
                                                                                                              Alignment Scores
                                                                                                                                                                                              expression modulating fragments of the S. pneumoniae genome. Products from the present invention can be used in diagnosis kits and assays, and pharmaceutical compositions and vaccines for S. pneumoniae.
                                                                                                                                                                                                                                                                                                            mrNA, DNA or cDNA produced from an organism, amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification primers derived from the fragment of the S. pneumoniae genome to prime the amplification and isolating the amplified sequences. The computer
                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid molecule is produced by a process comprising: (a) screening a genomic DNA library using as a probe a target sequence defined by any of the sequences in SEQ ID NO:1 to 391, identifying members of the library which contain sequences that hybridise to the target sequence and isolating the nucleic acid molecules from the members; or (b) isolating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Computer-readable medium with recorded Streptococcus pneumoniae polynucleotide sequences - useful in diagnostic kits and assays, pharmaceutical compositions and vaccines for Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus pneumoniae; computer readable medium;
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                                                                                       No . .
                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                     readable medium can be used in a computer-based system for identifying fragments of the S. pneumoniae genome of commercial importance, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus pneumoniae. The present invention also describes an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         recorded on it, or a representative fragment or a sequence at least 95% identical to SEQ ID NO: 1 to 391. The nucleotide sequences depicted in SEQ ID NO:1 to 391 (AAV52134 to AAV52524) are genomic fragments from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes a computer readable medium which has the nucleotide sequences SEQ ID NO:1 to 391 (AAV52134 to AAV52524)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 1379-1380; 1409pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       isolated nucleic acid molecule encoding a homologue of any of the fragments of the S.pneumoniae genome (SEQ ID NO:1 to 391) where the
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Rosen CA;
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IleLysAlaAlaValLysSerGlyIleLysAlaPheIleLysThrLeuValLysAlaIle 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus pneumoniae. The present invention also describes an Streptococcus pneumoniae. The present invention also describes an Streptococcus pneumoniae. The present invention also describes an Streptococcus pneumoniae genome (SEQ ID NO:1 to 391) where the Cfragments of the S.pneumoniae genome (SEQ ID NO:1 to 391) where the Cfragments of the S.pneumoniae produced by a process comprising: (a) screening a genomic DNA library using as a probe a target sequence defined by any Cf the sequences in SEQ ID NO:1 to 391, identifying members of the Clibrary which contain sequences that hybridise to the target sequence and isolating the nucleic acid molecules from the members; or (b) isolating Cf mRNA, DNA or cDNA produced from an organism, amplifying nucleic acid colored shows enucleotide sequence is homologous to amplification for primers derived from the fragment of the S. pneumoniae genome to prime Cf the amplification and isolating the amplified sequences. The computer creadable medium can be used in a computer-based system for identifying capacity of the S. pneumoniae genome. Products of computer in the present invention can be used in diagnosis kits and assays, and Cf pharmaceutical compositions and vaccines for S. pneumoniae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Computer-readable medium with recorded Streptococcus pneumoniae polynucleotide sequences - useful in diagnostic kits and assays. pharmaceutical compositions and vaccines for Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the nucleotide sequences SEQ ID NO:1 to 391 (AAV52134 to AAV52524) recorded on it, or a representative fragment or a sequence at least identical to SEQ ID NO: 1 to 391. The nucleotide sequences depicted sEQ ID NO:1 to 391 (AAV52134 to AAV52524) are genomic fragments from
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                                          TCAACAAGTGCCTCGGCTTCAGCAAGTACTAGCGCCTCAGCCTCAGCGTCAACAAGTGCT
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                                                                                                                                                       \verb|AlaProGlnGlnGlyValAlaAlaGlyLysGluSerSerGluSerGlnLysAlaGlyAla||
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    specifically claimed nucleotide sequences isolated from S. pneumoniae. The sequences have antibacterial and antiinflammatory properties. The protein sequences, and fragments of them, are useful as immunogens and/or antigens. The nucleotide sequences can be used in vaccines and in diagnostic assays. The proteins and nucleotides can be useful for the detection and diagnosis of S. pneumoniae. The protein sequences are also useful for screening an agent capable of antagonising, inhibiting or interfering with the function or expression of the proteins in which the agent is useful for treatment or prophylaxis of S. pneumoniae infection and meningitis. AAA05591 to AAA05614 represent primers used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  library which contain sequences that hybridise to the target sequence and isolating the nucleic acid molecules from the members; or (b) isolating mRNA, DNA or cDNA produced from an organism, amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification primers derived from the fragment of the S. pneumoniae genome to prime the amplification and isolating the amplified sequences. The computer readable medium can be used in a computer-based system for identifying fragments of the S. pneumoniae genome colours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expression modulating fragments of the S. pneumoniae genome. Product from the present invention can be used in diagnosis kits and assays, pharmaceutical compositions and vaccines for S. pneumoniae.
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                                                                                                                                                                                                                                                                                                                                      Streptococcus pneumoniae; vaccine; screening; protein antigen; antibacterial; antiinflammatory; meningitis; infection; diagno
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                                                                                                                                                                                                                                     Streptococcus pneumoniae
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5740	TCAGCAAGTACCAGCGCCTCAGCCTC	5699
397	LysAsnPheProLysLeuSerLysVallleSerSerLeuThrSerLysTrpValTh	378
5698	AGTACCAGCCTCAGCTTCAGCAAGCACCAGTGCGTCAGC	5654
377	laLysAlaIleSerLysGlyIleSerLysValPheA	358
357 5653	IleLysAlaAlaValLysSerGlyIleLysAlaPheIleLysThrLeuValLysAlaIle 	338 5597
σω	ValValGlnAlaValLysGlnAlaValIleThrAlaValArgGlnAlaIle	$\omega$ $\mu$
5 1	GlyAlaAlaGlyAlaAlaAlaAlaThrThrValAlaThrGlnIleThrValGlnA :::      :::      CCTCAGCAAGTACTAGTGCATCGGCTTCAGCAAGCACCAGTGCGTCGGCTTCAG	7 9
297 5476	CysGlyAlaGlyLeuAlaGlyLeuAlaAlaGlyAlaAlaValGlyA     	278 5417
277 5416	ThrValMetIleAlaValSerValAlaIleThrValIleSerIleValAlaAlaIlePhe :::	258 5357
257 5356	GluMetLysAlaAlaGluGlnLysSerLysAspLeuGluGlyThrMetAspThrValAsn :::    :::   AGTATCTCAGCGTCTGAATCGGCATCAACGAGTGCATCAGCATCAGCATCAACGAGTGCA AGTATCTCAGCGTCTGAATCGGCATCAACGAGTGCATCAGCATCAACGAGTGCA	238 5297
5296	AGTGCATCAGCATCAGCATCAACCAGTGCATCAGCCTCAG	5252
237	AsnLysLeuGlyLeuGluLysGlnAlaIleLysIleAspLysGluArgGluGluTyrGln	218
217 5251	GluAlaThrLysSerAlaLeuSerAsnTyrAlaSerThrGlnAlaGlnAlaAspGlnThr::::    ::::::                       :::: GCATCAACAAGTGCCTCAGCATCAGCATCAACGAGTGCGTCAGCCTCAGCAAGT	198 5198
197 5197	ProArgSerGluValIleGluIleGlyLeuAlaLeuAlaLysAlaIleGlnThrLeuGly:::	178 5138
177 5137	GlyLysSerSerGlySerAlaLysLeuGluThrProGluLeuProLysProGlyValThr:::	158 5078
157 5077	GlnSerLeuSerAlaAlaGlnMetLysGluValGluAlaValValValAlaAlaLeuSer	138 5018
137 5017	AlametGlnThrSerIleGluGluAlaSerLysSerMetGluSerThrLeuGluSerLeu	118 4958
117 4957	ValSerGlyAlaAlaThrThrAlaSerAsnThrAlaThrLysIle	102 4898
101 4897	uSerSerGluSerGlnLysAlaGlyAlaAspThrGly :::	82 4838
81 4837	pLysThrSerSerThrThrLysThrGluThrAlaProGln               : : : : : :       : : : : : : : :	62 4778
61 4777	LysGlnIleGlnGlnThrArgGlnGlyLysAsnThrGluMetGluSerAspAlaThrIle :::         :::       GCATCAACAAGTGCGTCGGCTTCAGCATCAACGAGTGCATCAGCTTCAGCATCAACAAGT	42 4718
4717	AGCGTCTGAATCA	4688

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The present invention describes a computer readable medium which has the nucleotide sequences SEQ ID NO:1 to 391 (AAV52134 to AAV52524) recorded on it, or a representative fragment or a sequence at least 95% identical to SEQ ID NO: 1 to 391. The nucleotide sequences depicted in SEQ ID NO:1 to 391 (AAV52134 to AAV52524) are genomic fragments from Streptococcus pneumoniae. The present invention also describes an isolated nucleic acid molecule encoding a homologue of any of the fragments of the S. pneumoniae genome (SEQ ID NO:1 to 391) where the nucleic acid molecule is produced by a process comprising: (a) screening a genomic DNA library using as a probe a target sequence defined by any of the sequences in SEQ ID NO:1 to 391, identifying members of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Computer-readable medium with recorded Streptococcus pneumoniae polynucleotide sequences - useful in diagnostic kits and assays, pharmaceutical compositions and vaccines for Streptococcus
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                                                                                                                                                                                                                                                                                                                                                              Claim 1;
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Streptococcus pneumoniae genome fragment
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                                                                                                                                                                                                                                                                                          Streptococcus
                                                                                                                                                                                                                                                                                                      computer
                                                                                                                                                                        Computer-readable medium with recorded Streptococcus pneumoniae polynucleotide sequences - useful in diagnostic kits and assays, pharmaceutical compositions and vaccines for Streptococcus
                                                                                                                                                                                                                                          31-OCT-1996;
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vaccine; pharmaceutical composition;
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on; ds.
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Claim 1; Page 575-593; 1409pp; English.

CC Streptococcus pneumoniae. The present invention also describes an CC isolated nucleic acid molecule encoding a homologue of any of the CC fragments of the S. pneumoniae genome (SEQ ID NO:1 to 391) where the CC nucleic acid molecule is produced by a process comprising: (a) screening CC a genomic DNA library using as a probe a target sequence defined by any CC of the sequences in SEQ ID NO:1 to 391, identifying members of the CC library which contain sequences that hybridise to the target sequence and CC library which contain sequences that hybridise to the target sequence and CC mRNA, DNA or cDNA produced from an organism, amplifying nucleic acid CC mclecules whose nucleotide sequence is homologous to amplification CC molecules whose nucleotide sequence is homologous to amplification CC primers derived from the fragment of the S. pneumoniae genome to prime CC treadable medium can be used in a computer based system for identifying CC from the present invention can be used in diagnosis kits and assays, and CC pharmaceutical compositions and vaccines for S. pneumoniae. recorded on it, or a representative fragment or a sequence at least identical to SEQ ID NO: 1 to 391. The nucleotide sequences depicted SEQ ID NO:1 to 391 (AAV52134 to AAV52524) are genomic fragments from The present invention describes a computer readable medium which the nucleotide sequences SEQ ID NO:1 to 391 (AAV52134 to AAV52524) ĺ'n

Sequence 32768 BP; 9834 A; 6168 C; 7154 G; 9609 T; 3 other;

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Best Local Similarity:
Query Match:
                       Percent Similarity:
                               Score:
                                               Alignment Scores:
                                        No.:
2.42e-05
213.50
37.33%
20.70%
9.01%
Mismatches:
Indels:
Gaps:
                        Length:
Matches:
Conservative:
 32768
107
86
256
69
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US-09-889-314-2 (1-496) x AAV52204 (1-32768)

- 밁 QΥ ACAAGCGCCTCAGCTTCAGCAAGTACCAGTGCGTCAGCCTCAGCGTCGACAAGTGCGTCG  ${\tt ThrAsnMetSerIleSerSerSerSerGlyProAspAsnGlnLysAsnIleMetSerGln}$ 21
- 22  ${\tt ValLeuThrSerThrProGlnGlnYValProGlnGlnAspLysLeuSerGlyAsnGluThr}$ 41

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RESULT 11
AAZO14
ID AAZO2
XX AAZO2
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28-NOV-1997;
17-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   trachomatis. Open reading frames (ORFs) of the genome encode polypeptides AAY36754-Y37949. The polypeptides can be used as vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences can all be used to control growth of the microorganism. Chlamydia trachomatis responsible for a large number of diseases, e.g. eye diseases such as conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion conjunctivitis; genital diseases such as nongonococcal urteritis; epidymitis, cervicitis, salpingitis, perihepatitis, bartholinitis; pneumopathy in breast feeding infants; and venereal lymphogranulomatosis. The polypeptides of the invention may be of use
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 TCGTTGTCATCTGTAGATGCCACGCATCTACAAGAAATTCAAAGCATCGTATCCTCTGCT
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                                                                    IleAlaMetGlnThrSerIleGluGluAlaSerLysSerMetGlu---SerThrLeuGlu
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                          GlyAlaAlaAlaThrThrAlaSerAsnThrAlaThrLysIleAlaMetGlnThrSerIle 123
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                                                                                                                                                                                                                                                                                                                                     ValAlaAlaGlyLysGluSerSerGluSerGlnLysAlaGlyAlaAspThrGlyValSer 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 ThrSerThrProGlnGlyValProGlnGlnAspLysLeuSerGlyAsnGluThrLysGln
                                                                                                                                                                                                                                                                                         GGAGCGGCTGCTACTACAGCATCAAATACTGCAACAAAAATTGCTATGCAGACCTCTATT
                                                                        LysGlnAlaIleLysIleAspLysGluArgGluGluTyrGlnGluMetLysAlaAlaGlu
                                                                                                    LeuSerAsnTyrAlaSerThrGlnAlaGlnAlaAspGlnThrAsnLysLeuGlyLeuGlu
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                                                                                                       C. pneumoniae polypeptide antigen variant fusion protein.

C. pneumoniae strain YK41 was cultured and genomic DNA extracted to prep. a lambda gtll DNA library. The library was then screened with an anti-YK41 monoclonal antibody (MAb), which was prepd. by fusing spleen cells from a mouse infected with YK41 with myeloma PJ/NS1/1-Ag4-1 to produce a MAb expressing hydridoma. The DNA COBACA31 to give pcpNS33T. The plasmid was used to transform an E. coli host, which was cultured to give an antigenic polypeptide from its DNA can be used in assays for the detection of the antigenic polypeptide antigenic polypeptide antibodies and DNA, respectively, useful in the diagnosis of C. pneumoniae infection.
                                                                                                                                                                                                                                                                                                                                                                                                                              28-APR-1995;
20-SEP-1994;
28-APR-1995;
28-APR-1995;
28-APR-1995;
28-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polypeptide antigen; strain YK41; plasmid; probe; pCPN533T; primer; assay; detection; antibody; diagnosis; infection; fusion protein; dihydrofolate reductase; DHFR variant; Chlamydia pneumoniae; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DHFR/C. pneumoniae antigen variant fusion protein
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                                                                                                                                                                                                                                                                                                                Recombinant Chlamydia pneumoniae antigen and antibodies to it used for detection and assay of C. pneumoniae e.g. in clinical
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95JP-0106006.
95JP-0106008.
95JP-0106009.
95JP-0106010.
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AAT14619

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      using
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DB; AAW01743.
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         GluValIleGluIleGlyLeuAlaLeuAlaLysAlaIleGlnThrLeuGlyGluAlaThr
                                     SerGlySerAlaLysLeuGluThrProGluLeuProLysProGlyValThrProArgSer
                                                                            SerAlaAlaGlnMetLysGluValGluAlaValValValAlaAlaLeuSerGlyLysSer
                                                                                                                GATACAAACATGTCTATTTCATCTTCTTCAGGACCTGACAATCAAAAAAATATCATGTCT
                            TCGGGTTCCGCAAAATTGGAAACACCTGAGCTCCCCAAGCCCGGGGTGACACCAAGATCA
                                                                   AGTGCCGCGCAAATGAAAGAAGTCGAAGCGGTTGTTGTTGCTGCCCTCTCAGGGAAAAGT
                                                                                                         ACCTCTATTGAAGAGGCGAGCAAAAGTATGGAGTCTACCTTAGAGTCACTTCAAAGCCTC
                                                                                                                                                                                                                                                                ACGAAGCAAATACAGCAAACACGTCAGGGTAAAAACACTGAGATGGAAAGCGATGCCACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and determination of anti-Chlamydia polypeptide C as the antigen
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Matches:
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20-SEP-1994;
28-APR-1995;
28-APR-1995;
28-APR-1995;
28-APR-1995;
The present sequence encodes a variant of the C. pneumoniae polypeptide antigen, polypeptide A. C. pneumoniae strain YK41 was cultured and genomic DNA extracted to prep. a lambda gtll DNA library. The library was then screened with an anti-YK41 monoclonal antibody (MAb), which was prepd. by fusing spleen cells from a mouse infected with YK41 with myeloma P3/NS1/1-Ag4-1 to produce a MAb expressing hydridoma. The DNA obtd. was then fused
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                                                                             Claim 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   C. pneumoniae
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                                                                                                       Recombinant Chlamydia used for detection and
                                                                                                                                    P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                               pCPN533alpha; primer; assay;
infection; variant; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   polypeptide antigen (polypeptide A) DNA variant.
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95JP-0106008.
95JP-0106009.
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94JP-0224711
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                                                                                                      pneumoniae antigen and antibodies to it assay of C. pneumoniae e \cdot g. in clinical
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C. pneumoniae polype
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Polypeptide antigen;
KW pcPN533alpha; primer
XW infection; clone; ds
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C. pneumoniae
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                                                                               US-09-889-314-2 (1-496)
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DB; AAR94586.
{\tt AspThrAsnMetSerIleSerSerSerSerGlyProAspAsnGlnLysAsnIleMetSerBerSerSerSerSerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerBerSerB
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                                                                                                                                                                                               CAACAGGGAGTTGCTGCTGGGAAAGAATCCTCAGAAAAGTCAAAAAGGCAGGTGCTGATACT
                                                                                                                                                                                                                                                                                                                                                                           ATTGCTGGTGCTTCTGGAAAAGACAAAACTTCCTCGACTACAAAAACAGAAACAGCTCCA
                                                                                                                                                                                                                                                                                                                                                                                  IleAlaGlyAlaSerGlyLysAspLysThrSerSerThrThrLysThrGluThrAlaPro
                                                                                                                                                                                                                                                       SerGlySerAlaLysLeuGluThrProGluLeuProLysProGlyValThrProArgSer
                                                                                                                                               TCGGGTTCCGCAAAATTGGAAACACCTGAGCTCCCCAAGCCCGGGGTGACACCAAGATCA
                                                                                                                                                                        GGTCTAGAAAAGCAAGCGATAAAAATCGATAAAGAACGAGAAGAATACCAAGAGATGAAG
                                                                                                                                                                             GlyLeuGluLysGlnAlaIleLysIleAspLysGluArgGluGluTyrGlnGluMetLys
                                                                                                                      ATCGCG
                                                                                                                                   IleAla 262
                                            antibody;
                                                                                              standard;
                               pneumoniae
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                                                                     (first entry)
                                                        pneumoniae
              Location/Qualifiers 236..1012
  /note=
        /*tag=
                                                                                              DNA; 1048
                                            detection;
 "no stop codon present"
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence ia an expression vector for the C. pneumoniae C polypeptide antigen, polypeptide A. C. pneumoniae strain YK41 was C cultured and genomic DNA extracted to prep. a lambda gtl1 DNA C library. The library was then screened with an anti-YK41 monoclonal antibody (MAb), which was prepd. by fusing spleen cells from a mouse infected with YK41 with myeloma p3/NS1/1-Ag4-1 to produce a MAb expressing hydridoma. The DNA obtd. was then fused with the expression vector pADA431 to give pCPNS33alpha. The plasmid was used to transform an E. coli host, which was cultured to give the antigenic polypeptide, polypeptide. Polypeptide A and primers and probes derived from its DNA can be used in assays for the detection of polypeptide A antibodies and DNA, crespectively, useful in the diagnosis of C. pneumoniae infection.
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                                                          AlaAlaGlnMetLysGluValGluAlaValValValAlaAlaLeuSerGlyLysSerSer
                                                                                                                                                                               ValSerGlyAlaAlaAlaThrThrAlaSerAsnThrAlaThrLysIleAlaMetGlnThr
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                                                                                                                     GCCGCGCAAATGAAAGAAGTCGAAGCGGTTGTTGTTGCTGCCCTCTCAGGGAAAAGTTCG
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	ULT 7	RES
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:valGlyLysLeuGlnAlaAlaAlaAspMetIleSerMe	429	Qy
ATGCCCGCGTTGCAGGCCATGCTGTCCAGGCAGGTAGATGACGACCATCAGGGAC	2036	Db
lnMetGlnLeuSerGluMetGlnGlnAsnValAlaGlnPhe 	409	Qy
TCGCCACGAGGCTGGATGGCCTTCCCCATTATGATTCTTCTCGCTTCCGGCGGCATC 20	7	B 4
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LysLeuSerLysValI1leSerSerLeu	382 1916	Db Oy
CACTGGTCCCGCCACCAAACGTTTCGGC 19	0	g Db
erLysGlyIleSerLysValPheAlaLysGlyThrGlnMetIleAlaLysAsnPhePro 381	36	Qy
TCGCTTGCGGTATTCGGAATCTTGCACGCCCTCGCTCAAGC	1826	Db
lyIleLysAlaPheIl	342	Qy
GTGCCGGCAGCGCTCTGGGTCATTTTCGGCGAGGACCGCTTTCGCTGGAGCGCG 1825	1772	
leThrAlaAlaIle······LysAla	332	Qy
CTTATGACTGTCTTCTTTATCATGCAACTCGTAGGACAG 1771	1733	Db
ThrValGlnAlaValValGlnAlaVa	312	Qy
AGAGCCTTCAACCCAGTCAGCTCCTTCCGGTGGGCGCGGGGCATGACTATCGTCGCCGCA 1732	1673	Дb
ThrThrValAlaThr 311	307	Qy
CTACTGGGCTGCTTCCTAATGCAGGAGTCGCATAAGGGAGAGCGTCGACCGATGCCCTTG 1672	1613	Db
306	306	Qy
GCGCCATCTCCTTGCATGCACCATTCCTTGCGGCGGCGGTGCTCAACGGCCTCAACCTA 1612	1553	Dр
	302	ОУ
GCTCATGAGCGCTTGTTTCGGCGTGGGTATGGTGGCAGGCCCGTGGCCGGGGGACTGTTG 1552	1493	Db
AlaAlaGlyGlyAlaAla 301	296	Qy
GTTGCTGGCGCCTA-TATCGCCGACATCACCGATGGGGAAGATCGGGCTCGCCACTTCGG 1492	1434	Db
AlaValGlyAlaAla 295	291	Qy
TANTCGATGATCCTCTACGCCGGGACGCATCGTGGCCGGCATCACCGGCGCCACAGGTGCG 1433	1374	DЬ
- 1	273	Оу
GCGAA-GGGGTTCGAATTGCCATGGGGGCCCCTTAATTAATTAACTCGAGAGATCCAGATC 1373	1315	Db
AlaIleThrVal	262	Qy
GCCGAACAGAAGTCTAAAGATCTCGAAGGAACAATGGATACTGTCAATACTGTGATGATC 1314	1255	Db
AlaGluGlnLysSerLysAspLeuGluGlyThrMetAspThrValAsnThrValMetIle 261	242	Qy
CTAGAAAAGCAAGCGATAAAAATCGATAAAGAACGAGAAGAATAACCAAGAGATGAAGGCT 1254	1195	Db
luArgGluGluTyrGlnGluMe	222	Qy
TCTGCCTTATCTAACCTATGCAAGTACACAAGCACAAGCAGACCAAACAAA	1135	Db
aLeuSerAsnTyrAlaSerThrGlnAlaGlnAlaAspGlnThrAsnLysLeuG	202	Qy

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                                                                                                                  IleAlaValSerValAlaIleThrVal----
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                                                                              AlaAlaValGlyAlaAla--
         CTACTACTGGGCTGCTTCCTAATGCAGGAGTCGCATAAGGGAGAGCGTCGACCGATGCCC 1888
                            TTGGGCGCCATCTCCTTGCATGCACCATTCCTTGCGGCGGCGGTGCTCAACGGCCTCAAC
                                       AlaGlyAla----
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                                                                                                                                       SerGlyIleLysAlaPheIleLysThrLeuValLysAlaIleAlaLysAlaIleSerLys 363
                                                                                                                                                                                                                                                                                                         GlnAlaValIleThrAlaValArgGlnAlaIleThrAlaAlaIleLysAlaAlaValLys
                                                                                                                                                                                                                                                                                                                              AlaAlaAlaThrThrValAlaThrGlnIleThrValGlnAlaValValGlnAlaValLys 323
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                                                                                    GluMetThrGlnLysAlaThrLysLeuGlyAlaGlnIleLeuLysAlaTyrAlaAlaIle 483
                                                                                                         SerLysValIleSerSerLeuThrSerLysTrpValThrValGlyValGlyValValValVal 403
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                                                                                                           Percent Similarity:
                                                                                                                                                                                            The present sequence ia an expression vector for the C. pneumoniae polypeptide antigen, polypeptide A. C. pneumoniae strain YK41 was cultured and genomic DNA extracted to prep. a lambda gt11 DNA ibrary was then screened with an anti-YK41 monoclonal antibody (MAb), which was prepd. by fusing spleen cells from a mouse infected with YK41 with myeloma P3/NSI/1-A94-1 to produce a MAb expression hydridoma. The DNA obtd. was then fused with the expression vector pADA431 to give pCPNB33alpha. The plasmid was used to transform an E. coli host, which was cultured to give the antigenic polypeptide, polypeptide A. Polypeptide A and primers and probes derived from its DNA can be used in assays for the detection of polypeptide A antibodies and DNA, respectively, useful in the diagnosis of C. pneumoniae infection.
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28-APR-1995;
28-APR-1995;
28-APR-1995;
28-APR-1995;
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                                                                                                                                                                                                                                                                                                                                                                        Claim 13; Pages 77-84; 128pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                  diagnosis
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P-PSDB; AAR94579.
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Conservative:
Mismatches:
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28-APR-1995;
28-APR-1995;
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pCPN533alpha; primer; assay; detection; antibody; diagnosi
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US-09-889-314-2 (1-496) x AAT14612 (1-1464)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence encodes the C. pneumoniae polypeptide antigen, polypeptide A. C. pneumoniae strain YK41 was cultured and genomic DNA extracted to prep. a lambda gtll DNA library. The library was then screened with an anti-YK41 monoclonal antibody (MAb), which was prepd. by fusing spleen cells from a mouse infected with YK41 with myeloma P3/NS1/1-Ag4-1 to produce a MAb expressing hydridoma. The DNA obtd. was then fused with the expression vector pADA431 to give pCPN533alpha. The plasmid was used to transform an E. coli flost, which was cultured to give the antigenic polypeptide, polypeptide A. Polypeptide A and primers and probes derived from its DNA can be used in assays for the detection of polypeptide A antibodies and DNA, respectively, useful in the diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnosis
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DB; AAR94579.
                                                                                                                                                               GlyAlaAlaAlaThrThrAlaScrAsnThrAlaThrLySIleAlaMetGlnThrSerIle
                                                                                                                                   ValalaalaGlyLysGluSerSerGluSerGlnLysAlaGlyAlaAspThrGlyValSer
                                                                       GGAGCGGCTGCTACTACAGCATCAAATACTGCAACAAAAATTGCTATGCAGACCTCTATT
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                      C. pneumoniae polypeptide antigen fusion protein, polypeptide B.
C. pneumoniae strain YK41 was cultured and genomic DNA extracted to prep. a lambda gtl1 DNA library. The library was then screened with an anti-YK41 monoclonal antibody (MAb), which was prepd. by fusing spleen cells from a mouse infected with YK41 with myeloma p3/NS1/1-Ag4-1 to produce a MAb expressing hydridoma. The DNA obtd. was then fused with DHFR DNA and the expression vector pADA431 to give pCPM533T. The plasmid was used to transform an E. coli host, which was cultured to give the antigenic polypeptide fusion protein, polypeptide B. Polypeptide B and primers and probes derived from its DNA can be used in assays for the detection of antigenic polypeptide antibodies and DNA, respectively, useful in the diagnosis of C. pneumoniae infection.
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28-APR-1995;
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20-SEP-1994;
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95JP-0106009.
95JP-0106010.
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US-09-889-314-2 (1-496) x AAT14618
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                                                                               SerValAlaIleThrValIleSerIleValAlaAlaIlePheThrCysGlyAlaGlyLeu.
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                               927740
                                                                                                                                                                                                                                                                                                                             The present sequence represents the complete genome of Chlamydia pneumoniae, and encodes proteins AAY345847-25879. C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAY34584-Y35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs
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21-NOV-1997;
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                                          IleAlaGlyAlaSerGlyLysAspLysThrSerSerThrThrLysThrGluThrAlaPro
                                                                                  ThrLysGlnIleGlnGlnThrArgGlnGlyLysAsnThrGluMetGluSerAspAlaThr
                               ATTGCTGGTGCTTCTGGAAAAGACAAAACTTCCTCGACTACAAAAACAGAAACAGCTCCA
                                                                      ACGAAGCAAATACAGCAAACACGTCAGGGTAAAAAACACTGAGATGGAAAAGCGATGCCACT
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence encodes a Chlamydia pneumoniae protein. The protein, immunogenic fragments of it, nucleotide sequences encoding it, or inhibitor specific against it are used to manufacturing a medicament for the treatment of infection due to C. pneumoniae. An antibody specific against the protein can diagnose a C. pneumoniae infection. C. pneumoniae infection can be prevented. Artherosclerosis, including coronary atherosclerosis, caused by C. pneumoniae can also be prevented or treated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New Chlamydia pneumoniae protein of 496 amino acids preventing and treating C. pneumoniae infection and including coronary atherosclerosis -
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360	1 AlaValLysSerGlyIleLysAlaPheIleLysThrLeuValLysAlaIleAlaLysAla	341	ОУ
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340	AlaValLysGlnAlaValIleThrAlaValArgGlnAlaIleThrAlaAlaIleLysAla	321	Qy
1020		961	Db
320	AlaGlyAlaAlaAlaAlaThrThrValAlaThrGlnIleThrValGlnAlaValValGln	301	Qy
960		.901	Db
300	AlaGlyLeuAlaGlyLeuAlaAlaGlyAlaAlaValGlyAlaAlaAlaAlaGlyGlyAla 	281 841	ф
280	IleAlaValSerValAlaIleThrValIleSerIleValAlaAlaIlePheThrCysGly	261	Qy
840		781	Db
260	. AlaAlaGluGlnLysSerLysAspLeuGluGlyThrMetAspThrValAsnThrValMet	24.	Qy
780		72.	Db
240	GlyLeuGluLysGlnAlaIleLysIleAspLysGluArgGluGluTyrGlnGluMotLys	221	Qy
720		661	Db
220 660	LysSerAlaLeuSerAsnTyrAlaSerThrGlnAlaGlnAlaAspGlnThrAsnLysLeu	60:	Db Qy
200	GluValIleGluIleGlyLeuAlaLeuAlaLysAlaIleGlnThrLeuGlyGluAlaThr	18:	Qy
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180 540	SerGlySerAlaLysLeuGluThrProGluLeuProLysProGlyValThrProArgSer	16: 48:	Оу
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-MODEL-frame+_p2n.model -DEV=x1h
-Q2-(Q2n2_1/USPPO_spool/US99889314/runat_24012003_144539_10097/app_query.fasta_1.647
-Q2-(Q2n2_1/USPPO_spool/US9889314/runat_24012003_144539_10097/app_query.fasta_1.647
-DB=LGENT-0-UNITS-bits -START-1 -END--1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALLIGN-45
-DOCALIGN-200 -THR_SCORE-pct -THRAMX=100 -THR_LENG-0 -MAXLENG-200000000
-MODE-LOCAL -OUTFMT-pto -NORM-ext -HEAPSIZE=500 -MINILENG-0 -MAXLENG-2000000000
-USER-US09889314_eCGN_1_1_125_erunat_24012003_144539_10097 -NOPU=6 -ICPU=3
-NO_XUPXY -NO_MMAP -LARGEQUERY -NEG_SCORES-0 -MAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS-1 -XCAPPOP=10 -XCAPPEXT=7
-YGAPPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

RES AAA  ID XX AC XX AC XX DT XX C XX XX T C XX XX XX XX XX XX XX XX XX XX XX XX X	0	NO. 100. 100. 100. 100. 100. 100. 100. 10
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(491 BP.  //  //  pneumoniae protein.  rein; infection; artherosclerosis  ss.  Oualifiers	AAF21607 AAAB1490 AAA31881 ABH068049 ABL06539 ABAU9498 AAV52502 AAL39666 ABL03131 AAI67647 AAS54978 AAV52396 AAV52396 AAV52501 ABU52396 AAV52501 ABU52501 ABU52501 ABU52503 ABU669245 AAH78245 AAH78245	ID  AAA63621  AAX91990  AAT14618  AAT14612  AAT14612  AAT14612  AAT14613  AAT14613  AAT14613  AAT14619  AAZ01425  AAV02204  AAV02204  AAV022496  AAAV022496  AAAV02500  AAA052486  AAV025160  AAA052497  AAAV03553  AAV02498  AAA08864  ABA073537  ABL17520
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3295 GAAGTAATT------GAAGCGAAACGCATCCTTGAGAAGGTAAAA 3333
                                                                                       3202 AATATCATTTCAAAA------AACGGTATAAACACCGTACTGTTAAAAGGC 3246
                                                                                                                                                                                                                                           400 GlyValValAlaAlaProAlaLeuGlyLySGlyIleMetGlnMetGlnLeuSerGlu 419 ::::::
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3201		314	В
399	7 IleSerSerLeuThrSerLysTrpValThrVal	38	Qγ
3141	GAGGCATCAGGTAACCATACAGTAGTGAATGCAACCAACGCAAATGGCTCCGGCAGCGTA	308	дь
386	7AlaL	37	Qy
3081	  2 AGCATTAACGCAAAC	302	Дb
376	6 SerLysValPh	36	Qy
3021		296	DЪ
365	6	34	Qy
2961	2 ATTACTTCAGCTAATAACCAGGTAAACCTTTCAGCTAAGGATGGTAGCATTGGGGGAAAT	290	Db
345	6 ValileT	32	Qy
2901	7 CTAACTGCAACATCGGGCAAATTAACCACTAAGGCTAGTTCAAGC	285	Дb
325	AlaThrThrValAlaThrGlnIleThrValGlnAlaValValGlnAlaVa	306	Qy
2856	GAGCCGC	284	망
305	6 LeuAlaAlaGlyAlaAlaValGlyAlaAlaAlaAlaGlyGlyAlaAlaGlyAlaAlaAla	286	Qy
2844	GGCGATTTAACTGTTGAA	2800	DЬ
285	AlaIleThrValIleSerI	266	Qy
2799	GCAA	2740	Db
265	LeuGluGlyThrMetA	249	Qy
2739	CAG	268	Дb
248	leAspLysGluArgGluGluTyrGlnGluMetLysAlaAlaGluGlnLysSerLysAsp	22	Qy
2682	GGCATGATTTCTGGTGGCAAAGTAGAAGTTAGCGCAAACCAAAGATTTA	262:	Вρ
228	JG1YLeuGluLysGlnAlaIleLys	211	Qγ
2622	ACCCAAGCAGGCTCTACGATTACTGGAACCGAGAGCGTGACCACTTCAAGCCAATCA	2566	Db
217	ThrLysSerAlaLeuSerAsnTyrAlaSerThrGlnAlaGlnAlaAspGlnThr	200	Qy
2565	ATAATTGGCGGTACAATTTCTGGTGGCACAGTAGAAGTTACCGCGACCGAAGGTTTAACC	2506	DЬ
199	VallleGluIleGlyLeuAlaLeuAlaLysAlaIleGlnThrLeuGlyGluAla	182	Qy
2505	GCAGACTCAAAAATTGAAGCGACTGAAGGCGAGGCTAATGTAACAAGCAAACAAGC	2449	Db
181	GlySerAlaLySLeuGluThrProGluLeuProLysProGlyValThrProArgSerGlu	162	Qγ
2448	GGCGGTAAAATTTCCGGCAAGACAGTAAACGTTAAAGCAACTAATAGTTTAACCACCCAA	2389	Db
161	AlaGlnMetLysGluValGluAlaValValAlaAlaLeuSerGlyLysSerSer	143	Qγ
2388	GCAGGCTCTACAATTAAAGGAACCGAGAGTATAACCACTTCAAGTCAATCAGGTAATATC	2329	Db
142	<pre>IleGluGluAlaSerLysSerMetGluSerThrLeuGluSerLeuGlnSerLeuSerAla</pre>	123	γо
2328	TCAGGCAACGCCGTTACTGCTACTGCAAATAGCGGTGCATTAACCACTTTG	2278	D
122	SerGlvAlaAlaThrThrAlaSerAsnThrAlaThrLysIl	103	2
277	TCCAAGCCTGGCTCTGTGACAATTGTGGCAGGCGGCGATACTCTTGCTGTAGGTAATATT	2218	J 2
102	GlvLvsGluSerSerGluSerGlnLysAlaGlyAlaAspThrGlyVal	87	Š

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Percent Similarity:
                                   Score:
                                                 Alignment Scores:
Pred. No.:
                                                                                                          ; NAME/KEY: CDS
; LOCATION: (127)..(7752)
US-09-702-251-3
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US-09-702-251-3
                                                                                                                                                                                                                                    Sequence 3, Application US/09702251
Patent NO. 6372492
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF TALIN EXPRESSION
FILE REFERENCE: RTS-0199
CURRENT APPLICATION NUMBER: US/09/702,251
CURRENT APPLICATION NUMBER: US/09/702,251
CURRENT FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 3
                                                                                                                                                               LENGTH: 8078
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        431 ValGlyLysLeuGlnAlaAlaAspMetIleSerMetPheThrGlnPheTrpGlnGln 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      391 ThrSerLysTrpValThrValGlyValGlyValValValAlaAlaProAlaLeuGlyLys 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               411 GlyIleMetGlnMetGlnLeuSerGluMetGlnGlnAsnValAlaGlnPheGlnLysGlu 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             357 IleAlaLysAlaIleSerLys-----GlyIleSerLysValPheAlaLysGlyThrGln 374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCCGGCCAGCCGGTGGTCCTCGACGTCGCCGCCGGCGGCATCGATATCGCCAGCCGCAAG 3479
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                               Length: Matches:
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LLysGlnAla            :  :::::::::::::::::::::::	Thrva:	laGlyA ACAGTG	ATCCTAGCTG	TGATGCTGAGGGGG		TGGGAC	ACACCA	lnThr/	AGCATGTG		TTG		euALaI ::	TACA	ProGluI	 CTGCAGCAACAC	aLeu-	GCC Ees	AGGATO	InThre	CCAGGCCAGTGGGG	rGly\	CAGCC	oGlnc	TGTTG	rIle#	(1-4	larity.
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leThrAlaVa :::    CTCAGCCAC	hrValAlaThrGlnIleThr     ATGCAGCTGCGCAGAATGCC!	LyAla <i>i</i>      CAGCAC	GATGCCACAGCCAAGA	TGATO	etAsp]	rccrec	CACTG	LyLeuGlul	\TGCC#		SAGCAG		nThri	ij.	ດ	CCTAT		aAlaGlnMe         GGCCCAGCG	GCTCG	uAlas	TGTTG	aAlaA	CCCGT	aAlaG	III AGGGC	rGlvL	9-702	
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gGlnAlaIleThrAlaAl              -CAGACCATCGCTGCAGC	AAGAAAAAGCTG	lyAlaAlaAlaAlaGlyGlyAlaAla                   :::  CAGCAGCGGCTGCGGGAGGCAGCTGA	ATGGTAGAGGCTGCCAAGGGA	AACTC	tAspThrValAsnThrValMetIleA	0	ATCTTT	pGlnThrAsnLysLeuGlyLeuGluLysGlnAlaIleLysIleAs	AGGGCTGGGCCTGCTGGCC		AGGGGTAGGAGCAGCAGCAGCTGTCACCCAGGCC	TyrAl	aLeuAlaLysAlaILeGInThTLeuGIyGLuAlaThTLySSerAlaLeuS 	GTCTGCCAAGAGCAACTGGTGG	lyValThrProArgSerGluValIleGluIleGly	TGTGCCCTATCCACTTCCCAACTAGTGGCCTGTACTAAGGTGG	SerGlyLys	GAGGAC	AGGATGCGCTAATGCAGCTCGCCAAAGCTGTGGCAAGTGCTGCAGCTGCCCTG	SerMet	AATT	ThrAla	AGCCAGTGCTGAGCCCCGTCAGAACCTGCTGCAAGCAGCTGGGAACGTGGG	roGlnGlnGlyValAlaAlaGlyLysGluSerSerG		LysThi	3 (1-8	Mismatches Indels: Gaps:
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hrala      CTGCA	-ValGlnA         GTGCAGC	LAALAG :: I SCTGAG	CAAGG	GCTC-	tIleA	CCTGG	CATGG	/SIle#	TGGCC		CCAGG	ırGlna	SSETA	ACTGG	.uValI	GGCCI	rSerGlySerAl	-Valg	TGCTG	luSerThrLeuGluSer	GGGGAAAGTGATACTGACCC	nThra	CAGCT	luSerG	l CAGAA	rThrT		19 81 16
aIl   TC#	G 1	laGlyAlaAla- <i>l</i>            GAGGGGCTGCGC <i>l</i>	9	- 1		TCAAT	16	_Iq	GTTATG	;	Ç	la	TaLeu   i	TGGAG	leGlu	GTACT	erAla	ValGluAlaValVa :::::: CTTCAGACCCAAGT	CAGCT	euGlu	ATACT	laThr	GGGAA	lnLys	CTGCT	hrLvs		œ
.eLysal     GCACGC	va le GAGC	Ala-A     GCGCA	CTGC	AGTGC	aValSerVal	➣	ATGCTGG	lua	GACCAG	Gln	ATG	; ;	era era	AGGCTGGAC	IleGl	AAGGT	aLysLeuG	ValVa    CAAGT	GCCCT	Ser	GACCC	ro.	CGTGG	erGlnLysAlaGlyAl	GCGCA	ThrGl		
LaAl       CAGC	lnAl     ATGC	laAl    TGGC	CCAC	200	LAla 	AAG	GGGAG	= 1	GCT	Ala	TG	; 8	1000 1000	CGA	Leu	G	lu	Val ::: ATT	GTC	!	CCAC	ileAla	;	Ala	TGC	Thr		
341 2942	321 2885	306 2825	7	2706	6	σ	249	ω 4	2529	214	A 1	12	2409	υ	187	2295	167	153 2235	2175	136	2115	118	2060	98		78		

## Tue Jan 28 10:21:43 2003

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Alignment pred. No.: Score: Percent Si Best Local	SULT ABBATAS ARZU, TTTIOLOG NU CU	459 3478 467 3535	3358 451 3418	68 11 98	357 I 3151 T 375 - 3211 G 391 T	134 137 191	295 - 2914 T 298 G 2974 G 317 A	294 2854 CT
Score milaı   Sim	ANT OF THE STREET	ThrGlyGluSe       GGCGAGCG GlnLysAlaTh ::::::	GCGGACAACC' AlaSerLys-	CAGGCCGGT		ପ୍⊹ଦ ହ	TACGGTTACGJ GlyGlyAlaA:     	GGTGC
es: city: llarity:	1183745 WT: DANCHIN, P. TIEN; LADANT, I. F. INVENTION: P. SES USES USES APPLICATION I. APPLICATION NUMBER CATION N	LaT	GCGGACAACCTGAAATCCGTC AlaSerLys	AGGCCGGTTGGAACGCCAGCGTG  (LY11eMetG1nMetG1nLeuSerG1u        : : : :         : : :         : :	AlaLysAlaIleSerLys-     :::		ACGGTTACGAGGGGG ACGGTTACGAGGGGGG LLYG1YA1AA1aG1YA LLILILI LLILILI GCGCCGTCGCCGCG	AGCAATCGC
0.00020 147.50 32.47% 19.69%	ANTO DANI ADEN 13 13 DATA DATA 1: U	erAsnGluMetThr :::   :::   GGCCGGCGCTGACGTTC hrLysLeuGlyAlaGln	HATCCGTCGAC	TGGAACGCCAGCAGCGTG GInMetGInLeuSerGlu :::::   ::: ;ACGACAGAGATCTCCAAG	AlalleSerLys AAGATCGACGAGCTGGGMetlleAlaLysAs :::              GAACAACTGGCCAA  GTPValThrValGlyVa	AGCGTGGTA AlaAlaValLys ::::: GGCATCCTGCGG	GACGCCTTGC AlaAlaAlaAlaA :::   CGTCTCCGCCG	ACT
)204 7#	INE, GLASER, EL, ULLMAN, YL CYCLASE : : S/08/426,54	luMetThr :::   cccrgacGTTC ceuGlyAlaGln      ccgGCCAAGAGC	GACG	CCAGCAGCGTG LnLeuSerGluMe ::::   :: ;AGATCTCCAAGTC	sGl; ; GCTGGGCGG aLysAsnPl             CAATTG LGlyValG:	GGGGCCC SerGlyI	TTGCTGGC	ATC
Lengt Match Conse Misma	□ □>	A, Le	TTCGTGGACCGC		GlyIleS GGCGGGCCGC AsnPheProL	::: CGGTGGCG [leLysAla ::: CAGCAGCCC	CCCAGCTThrTh :::   TGAGCAC	GCTGG
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ve :	g; KRIN,	aA GCG	TTCGTCCP	ALALAGL ::     GGCCGC	TPHEALO	CACTTCC CELYSThr	GACAAG ThrGln GCCGCG	CAG
1443 114 14 210	EVELYN	AGG AII aII	TCCAGGGCGAG	lnPheGln CCATTACC	rLysvalFireALDLysvalFireACTGC AGCGTACTTCGAGAAAAACCTGC 'SLeuSerLysvalIleSerSerL	GTGGTCACCTTCCTTGCTGACC  PhelleLysThrLeuValLys          : : :          ATCATCGAAAAGCTGGCCAAC	ACAAGACGCCGCCG hrGlnIleThrValG :::::::: CGGCGGTGTCGATCG xrgGlnAlaIleThrA	AATCG
	4,	GCA Y 4 C 3	GAGCGGGTG SerLysGln SerLysGln SerCGCAAG	;lnLysGlu ;lnLysGlu ;CCGGCAAC	CTGCAG SerLeu      CTGCAG	GG ATT		AGCGCA 2
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Qy 294 Db 2856 CTGGTGCAG	Qy 287 AlaAlaGly? :::       Db 2796 TCGGCCGGG	Qy 267 IleThrVallleSer ::: ::: ::: Db 2742 TTGGCGCTGGCCGCG	247 I 2697 I	227 2637	207 T	187 L 2574 T	2565	167	147 2505		9	109	102 ValSerGlyAl             1	82 GlnGlyValAla     ::: 2286 CAAGTCTTGCA	62 AlaGlyAlaSer     ::: 2256 GTGGAAGCGGCC	42 LysGlnIleGln 2199 CTTGATGGGGTG	29 2145 TTGCGGCGGCCG	12 ProAspAsnGln       2085 CCGAGCGGACGT	09-889-314-2 (1-496	y Match:
GGTGCAGCAATCGCACTATGCGGAT	AlaAlaGlyAlaAlaValGlyAla :::            rcggccgggcggcTgccggcgcATTggccgcggcgcTcAGTCCCATGgAGATCTACGGC	IleThrVallleSerIleValAlaAlaIlePheThrCysGlyAlaGlyLeuAlaGlyLeu   ::	LysAspLeuGluGlyThrMetAspThrValAsnThrValMetIleAlaValSerValA.la 	TleLysIleAspLysGluArgGluGluTyrGlnGluMetLysAlaAlaGluGlnLysSer :::	yrAlaSerThrGlnAlaGinAlaAspullillAsulysbowers	LeuAlaLeuAlaLySAlaIleGInTRLEUSIYOTUATETTTI :::		GluThrProGluLeuProLysProGlyValThrProArgSerGluValIleGluIleGly	GluvalGluAlaValValAlaAlaLeuSerGlyLysSersEFG1YearAcatysaca 	:::     :::     :::     :::       :::	rThrLeuGluSerLeuGl	ThrAlaSerAsnThrAlaThrLysIleAlaMetGlnThrSerIleGluGluAlaSerLys	ValserGlyAlaAlaAla	GlnGlyValAlaAlaGlyLySGluSerSerGlUSerGInLySALdolyAldasy************************************	AlaGlyAlaSerGlyLysAspLysThrSerSerThrThrLysThrGlullLAlact.Col.	LysglnIleGlnGlnThrArgGLnGIYLYSASnTHL Clumetor ::::    CTTGATGGGGTGGGATCGCGATCGTTCTCGTTGGGCGAGGTG-	TIGCGGCGCCGTCGCTGGGCGCAACGCAACGCAGAT	LysAsnIle TCGAAGTTC	) x 5183745-5 (1-6	6.23% I
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CGCAGGAATCGAGCGC	CCATGGAGATCTACGG	laGlyLeuAlaGlyLeu :::        GCAGGTGGCCGGGGCG	eAlaValSerValAla          :::     GGCTTCTTCCATCGCG	aAlaGluGlnLysSer	GCCGGG	CGCGGCCGTTGGC	CONTRIBUTED ASI	valileGluileGly     	GGGTCTTCGCGCTGG	GTGTTCGGCTTGGGC	GlnMetLys	GluGluAlaSerLys     	GCCCAGGCGGTGGCG				•			р
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• sp									RESU US-0 ; Se ; Pa ; G	Оy	Db Qy	Оy	Оy	Оy	DЬ
OTHER INF OTHER INF OTHER INF OTHER INF 08-669-785-1	STRANDEDN TOPOLOGY: MOLECULE TY FEATURE: NAME/KEY:	INFORMATION SEQUENCE C LENGTH: TYPE: n	NAME: Mey REGISTRATI REFERENCE/ TELECOMMUNIC TELEPHONE: TELEFAX:	APPLICATION   FILING DATE: CLASSIFICATIO ATTORNEY/AGENT	MEDIUM TX COMPUTER: OPERATING SOFTWARE:	COUNTRY: ZIP: 20 COMPUTER R	ADDRESSEE: STREET: 1 CITY: Was	APPLICANT: APPLICANT: APPLICANT: TITLE OF I TITLE OF I NUMBER OF	RESULT 42 US-08-669-785-1 ; Sequence 1, A ; Patent No. 63 ; Patent No. 63 ; GENERAL INFO	467 Glr ;;; 2740 CGC	459 Thr 2683	451 Ala       2623 GCC	431 Val 2563 GCC	411 Gly      2503 GGC	2473 CAG
INFOR INFOR INFOR	EDNESS: GY: lin TYPE: EY: CDS	ON FOR SEQ ID E CHARACTERIS H: 6441 base nucleic aci	eyers TION E/DOC ICATI	0 2;		Y: USA 20005-33 READABL	SSEE: Finne 1: 1300 I S Washington	APPLICANT: Sebo, Peter APPLICANT: Guiso, Nico TITLE OF INVENTION: Pr TITLE OF INVENTION: Cy TITLE OF INVENTION: Th NUMBER OF SEQUENCES: 4	R 099	GlnLysalaThrLysLeuGlyAlaGlnIleLeuLysalaTyrAlaAlaIleSerGly ::::::	ThrGlyGluSerAsnGluMetThr	AlaSerLys1leAlaSerLysGln     ::: 	ValGlyLysLeuGlnAlaAlaAlaAspMetIleSerMetPheThrGlnPheTrpGlnGln ::: GCGGACAACCTGAAATCCGTCGACGTGTTCGTGGACCGCTTCGTCCAGGGCGAGCGGGTG	GlyIleMetGlnMetGlnLeuSerGluMetGlnGlnAsnValAlaGlnPheGlnLysGlu     ::: 	:::       CAGGCCGGTTGGAACGCCAGCAGCGTG
	doub ear ONA (	a da El C	, Kenneth J. NUMBER: 25,1 NUMBER: 25,1 KET NUMBER: ON INFORMATIO 202) 408-4400	UMBER: US/0 27-JUN-1996 N: 424 INFORMATION:	TIPE: FIOPPY GISK ER: IBM PC COMPATIBLE ING SYSTEM: PC-DOS/MS RE: PatentIn Release	5 FORM		peter peter protection	on	ırLysLeuGl          GAAAACGGC	CASNGluMe :: CCGGCGCT	GTGGTCCT	uGlnAlaAl  ::::: GAAATCCGT	MetGlnLe ::::: ACAGAGAT	AACGCCAG
/note= "AMINO CORRESPONDING CODING FOR THE	omic)	rs 1:	ώ 5	US/08/669, 1996	oy disk compatible PC-DOS/MS-DOS Release #1.0		Henderson	ective E lase-Haem	US/08669785	yAlaGlnI    CAAGAGCG	tThr :    GACGTTCA	CGACGTCG	aAlaAspM CGACGTGT	uSerGluM :   ::: CTCCAAGT	  CAGCGTG
INO ACID SE ING TO THE THE B. Per			6.0072-00	785	)S 0, Version		n, Farabow, Suite 700	er:  Cole  Protective Epitopes Of Aden  Cyclase-Haemolysin(AC-Hly),  The Treatment Or To The Pre		leLeuLys; AATTCACC;	TCACGCCG	ccecceec	etIleSer ;;; TCGTGGAC	etGlnGln <i>I</i> CGGCGCTC	
ACID SEQUENCE TO THE NUCLEOTIDE B. Pertussis AC-			00000		on #1.30		w, Garrett	Of Adenyl C-Hly), T The Preve		AlaTyrAla ::: ACATTCGTO	TIGGCCGCC	GCATCGAT	detPheThr      GCTTCGTC	\snValAla :::    ;AACTGGCC	
TIDE AC-H							tt & Dunner	heir		AlaIleSe      GAGATCGT	CCAGGAGA	·IleAlaSerLysGln          :::::: !ATCGCCAGCCGCAAG	GlnPheTr     CAGGGCGA	GlnPheGl GCCATTAC	
SEQUENCE OF							ler	Application To		rGly 485      GGGC 2796					ATC
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to.								Infections.				,			

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AlaAlaGlyAlaAlaValGlyAla::::	/ IleThrValIleSerIleValAlaAlaIlePheThrCysGlyAlaGlyLeuAlaGlyLeu :::	LysaspleuGluGlyThrMetAspThrYalAsnThrYalMetLeAlaYalSerYalAla 	IleLys   IleAspLysGluArgGluGluTyrGluGluMetLysAlaAlaGluGluThySser	GCCGGG	${\tt TyrAlaSerThrGlnAlaGlnAlaAspGlnThrAsnLysLeuGlyLeuGluLysGlnAla}$	LeuAlaLeuAlaLysAlaIleGlnThrLeuGlyGluAlaThrLysSerAlaLeuSerAsn :::    :::    :TTCGGCGTGGCTGGCGGCGCATGGCGCTGGGAGGCGGCATCGCCGCGGCCGTTGGC	GCCGGCGGT	GluThrProGluLeuProLysProGlyValThrProArgSerGluValIleGluIleGly	GluValGluAlaValValValAlaAlaLeuSerGlyLysSerSerGlySerAlaLysLeu	SermetGluSerThrLeuGluSerLeuGlnSerLeuSerAlaAlaGlnMetLys :::	cc ys	ត ។	GlnGlyValAlaAlaGlyLySGluSerSerGluSerGlnLysAlaGlyAlaAspThrGly	AlaGlyAlaSerGlyLysAspLysThrSerSerThrThrLysThrGluThrAlaProGln	LysGlnIleGlnGlnThrArgGlnGlyLysAsnThrGluMetGluSerAspAlaThrIle 6 :::    :::    CTTGATGGGGTGGGATCGCGATCGTTCTCGTTGGGCGAGGTGTCCGACATGGCCGCC 2	TTGCGGCCGTCGCTGGGCGCAGTGGAACGCCAGGATTCCGGCTATGACAGC	GlnLysAsnIleMetSerGlnValLeuThrSerThrProGln::: :::        :::     CGTTCGAAGTTCTCGCCGGATGTACCTGGAAACGGTGCCGGCGTCACCCGGA	-314-2 (1-496) x US-08-669-785-1 (1-6441)	gnment Scores:       0.000204       Length:       6441         d. No.:       147.50       Matches:       114         re:       147.50       Conservative:       74         cent Similarity:       19.69%       Mismatches:       210         t Local Similarity:       19.69%       Indels:       181         ry Match:       4       Gaps:       22
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Sequence 377, Application US/08961527
Patent No. 6420135
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus p
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                  RESULT 40
US-08-961-527-377
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E: Human Genome Sciences,
9410 Key West Avenue
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 20850
COMPUTER READABLE FORM:
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LENGTH: 690 base pairs
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STRANDEDNESS: doub
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OPERATING SYSTEM: MSDOS ve
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                                      LeuGlyGluAlaThrLysSerAlaLeuSerAsnTyrAlaSerThrGlnAlaGlnAlaAsp 215
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                     GAATCGCCATCAACGAGTGCGTCGGCCTCA-----
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                                                                                                                                     ValThrProArgSerGluValIleGluIleGlyLeuAlaLeuAlaLysAlaIleGlnThr 195
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Qy 99 pThrGlyValSerGlyAlaAlaThrThrAlaSerAsnThrAlaThrLySIleAlaMe 119	ENTION: VECTOR SYSTEMS GOURNCES: 4 CCE ADDRESS: 4 CCE ADDRESS: 4 U.S.A. U.S.A. U.S.A. U.S.A. EN PC COMPACTIBLE SYSTEM: PCT-DOS/MS-DOS PATENTIN Release #1.0, V. LICATION DATA: DOCKET NUMBER: PCT/US93/03993 TE: 19930428 ATION: LICATION INFORMATION: LICATION INFORMATION: LICATION INFORMATION: 1713/651-5246 5280 FOR SEQ ID NO: 1: ARACTER ACID ESS: double 11:0ear PE: DNA (genomic) LICATOR ACID LIC	T :: ::

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Sequence 1, Application US/08458240
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                                                                                                                                                           TGGCGGCGGCGGCTCCCAACAGTATCAGTGCCAGAGCTACGGAGGCGGTTCTAG 3538
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION: APPLICANT: ROOP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 07/876,286
FILING DATE: April 30, 1992
APPLICATION NUMBER: NO. 6143727
FILING DATE: October 29, 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Rothnagel, Joseph A.
APPLICANT: Greenhalgh, David A.
TITLE OF INVENTION: SPECIFIC EXPRESSION VECTORS
                                                                                                                                                   2608
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OPERATING SYSTEM: IBM MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: SPECIFIC EXPRESSION TITLE OF INVENTION: AND METHODS OF USE
2727 CCCTGCCCTCCTGTGGGTTGTGGAAAGACCTCTGGTGGAGGAGGAGGCGGCGGCGGCTAT 2786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 611 West
CITY: Los Angeles
STATE: California
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ZIP: 90017
                                                                                                                                                                                    57 SerAspAlaThrIleAla-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Warburg, Richard J. REGISTRATION NUMBER: 32,3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/458,240
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                                                                          TTCTTCCAGGGTTCCCCTTCTCCTTA-AACAAGATGTCTCACCAGAAAAAAGCAGCCCACT 2726
                                                                                                                                                   GCATCTGCCACCTTCACAGCGTCCTCTTGCTGCTGTTGGTCTAATGTTGCTCTTCTGCTC 2667
                                 ProGlnGlnGlyValAlaAlaGlyLysGluSerSer-GluSerGlnLysAlaGlyAlaAs 99
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RESULT 37 US-08-146-930-1

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1666 GATGACGCGCCGGCCGGACAGAAGGCCGCCGCCGCCGCGCGAGATCGCGCTGCAGTTGACA 1725
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                                                                                                        CCGGCGCTGACGTTCATCACGCCGCCTGGCCGCCAGGAGAAGAGCAGCGCCGCGCGCACG
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Patent No. 5958764
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APPLICANT: Roop,
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INFORMATION FOR SEQ ID NO:
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APPLICANT: Greenhaldh, David A.
TITLE OF INVENTION: SPECIFIC EXPRESSION
TITLE OF INVENTION: AND METHODS OF USE
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
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CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
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                                                                                                                                                                                                        2548 AATGGAGTCCAGACACCTAGTCTGCATAAAGCTAGGAGTCAGAAGTATGTTGGCATGGAT
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OPERATING SYSTEM: IBM MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
                                                    2668 TTCTTCCAGGGTTCCCCTTCTCCTTA-AACAAGATGTCTCACCAGAAAAAGCAGCCCACT 2726
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: singl
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Rothnagel, Joseph P.
Greenhalgh, David P.
INVENTION: SPECIFIC E
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US-08-669-785-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No. 6309648
GENERAL INFORMATION:
APPLICANT: Betsou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3,
                      APPLICATION NUMBER: US/08, FILING DATE: 27-JUN-1996 CLASSIFICATION: 424 ATTORNEY/AGENT INFORMATION: NAME: Meyers, Kenneth J. REGISTRATION NUMBER: 25,14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1109
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                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Protective Epitopes Of Adenyl
TITLE OF INVENTION: Cyclase-Haemolysin(AC-Hly), Their Application To
TITLE OF INVENTION: The Treatment Or To The Prevention Of Bordetella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                       CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
      REFERENCE/DOCKET NUMBER:
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Guiso, Nicole
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Best Local Similarity:
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LENGTH: 5118 base pair
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                                             GGCGGCGCGATGGCGCTGGGA-
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APPLICANT: LYND DOUCETTE-Stamm et al
APPLICANT: LYND DOUCETTE-STAMM et al
APPLICANT: LYND DOUCETTE ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: NUCLEIC ACID AND DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1997-08-13
PRIOR APPLICATION NUMBER: US 60/054,964
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 1685
LENGTH: 3561
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; ORGANISM: Staphylococcus epidermidis
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SEQ ID NO 1626
LENGTH: 6414
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CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
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                                                                                                                                                                                                           MetLysGluValGluAlaValValAlaAlaLeuSerGlyLysSerSerGlySerAla 164
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                                                                      IleGlyLeuAlaLeuAlaLysAlaIleGlnThr---LeuGlyGluAlaThrLysSerAla
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CGATCCGCCGCCGCCGCCACC-
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                                         GCCGCCACAGCTAGAGCCGCCGCCTGCTTCCACCGCC-----
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                                                                   AlaThrGlnIleThrValGlnAlaValValGlnAlaValLysGlnAlaValIleThrAla 329
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US-09-134-001C-1515/c
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Best Local Similarity:
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
TITLE OF INVENTION: EDIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/054,964
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 1515
SEQ ID NOS: 5674
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                                                                      AAAGCGAGCGAATCAGCAAGCACAAGTAAACTATTATCAGAATCAGTGAGTACGTCGACG
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                                                                                                                                                                           AlaAlaAlaThrThrAlaSer---AsnThrAlaThrLysIleAlaMetGlnThrSerIle 123
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TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1
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FILING DATE: April 30, 1992
APPLICATION NUMBER: NO. 6143727 yet assigned (204/132)
FILING DATE: October 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 204/152
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
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LENGTH: 6530 bases
TYPE: nucleic acid
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APPLICATION NUMBER:
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                                                                                                                                                                             {\tt ThrProArgSerGluValIleGluIleGlyLeuAlaLeuAlaLysAlaIleGlnThrLeu}
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APPLICANT: Greenhalgh, David A.
TITLE OF INVENTION: SPECIFIC EXPRI
TITLE OF INVENTION: AND METHODS OF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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FILING DATE: April 30, 1998
APPLICATION NUMBER: No. 5958764 your print of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the prior of the p
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TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Warburg Pitt
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
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TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
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LENGTH: 6530 bases
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CITY: Los Angeles
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 20
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Ld A.
FIC EXPRESSION '
TODS OF USE
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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US-08-458-240-1/c
                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08458240 Patent No. 6143727
                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3773
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                                                                                                                                                                                                APPLICANT: Roop, Dennis R.
APPLICANT: Rothnagel, Joseph A.
APPLICANT: Greenhalgh, David A.
TITLE OF INVENTION: SPECIFIC EXF
TITLE OF INVENTION: AND METHODS
                                                                                                                                                                                                                                                                                                                                                                 3236 GCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      290 AlaAlaValGlyAlaAlaAlaAlaGlyGlyAlaAlaGlyAlaAlaAlaAlaThrThrVal 309
                                                                                                                                                                NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Di
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                                                                                                                                                                                                                                                                                                                                                                                             370
COMPUTER:
OPERATING
SOFTWARE:
                                                                                                      STREET: 611 West;
CITY: Los Angeles
STATE: California
                                                                         ZIP:
                                                                                         COUNTRY:
                                                                                                                                                   ADDRESSEE:
                                              MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AspLysGluArgGluGluTyrGlnGluMetLysAlaAlaGluGlnLysSerLysAspLeu
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                                                                                                                                     E: LYON & LYON
611 West Sixth
 SE: 3.0 COMPATIBLE STORM IBM MS-DOS (Version 5.0)
                                                                                         U.S.A.
                                                                                                                                                                                                                                                           Dennis R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -ACCGCTAGAACCGCCTCCGTAGCTCTGGCACTGATACTGTTGGGA 3498
                                                Diskette, 1.44 Mb storage
                                                                                                                                          Street
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d A.
IC EXPRESSION VECTORS
OF USE
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US-08-591-079-5
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                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                    US-09-889-314-2 (1-496) x US-08-591-079-5 (1-3106)
                                                                                                                                                                                                                                                                                                          Query Match:
                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores: Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-591-079-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/08591079
Patent No. 5972899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0764
TELEX: 90-4030 MRSNFOERSWSH
INFORMATION FOR SEQ ID NO: 5:
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LENGTH: 3106 base pairs
TYPE: nucleic acid
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Livnat, Shruel
REGISTRATION NUMBER: 33,949
REFERENCE/DOCKET NUMBER: 15661-20017.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Zychlinksky, Arturo
APPLICANT: Chen, Yajing
                                                                                                                                172 ProLysproGlyValThrProArgSerGluValIleGlu---IleGlyLeuAlaLeuAla 190
                                                                                                                                                                                                               152 ValValAlaAlaLeuSerGlyLysSerSerGlySerAlaLysLeuGluThrProGluLeu 171
                                                                      191 LysalaileGln-----ThrLeuGlyGlualaThrLysSerAlaLeuSerAsnTyrAla 208
                                                                                                                                                                               111 GTCGCGGGAGAACTGAAGGATAAAAATGGCGGGGTGAGTTCT---CAGGGCGTACAGCTC 167
     209 Ser---
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: CDS
LOCATION: 12..1217
OTHER INFORMATION:
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CLASSIFICATION: 435
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OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: MORRISON & FOLIAGE NW STREET: 2000 Pennsylvania Avenue, NW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                            CCTGCACCACTAGCAGTTGCCAGCCAAGTTACTGAAGGACAACAGCAAGAAGTCACT 227
                                     AAATTATTGGAGTCGGTCACCCGCGGCGCGGCGGCAGGATCTCAACTGATATCAAATTATGTT 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20006-1812
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152.50
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23.43%
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10
   --ThrGlnAlaGlnAlaAsp------GlnThrAsnLys 219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US/08/591,079
                                                                                                                                                                                                                                                                                                          Conservative: Mismatches: Indels:
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Matches:
                                                                                                                                                                                                                                                                                          Gaps:
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56
163
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	GENERAL INFORMATION: APPLICANT: Roop, Dennis R.	GENER/ APPI		
	)  -930-1/c  -930-1/c	SULT 30 S-08-146-9 Sequence	RES US-	
	ATTRATGCAAAAGGTGACATGCTGCATAATTTGGCCGGCAGACCCCCATACT 1211	1161	Db	
		477	Qy	
116	GAAGAGTTATCCCATTTGTCAGAGTCACATCAACAAGTGATGGAACTGATTTTCCAGATG	1101	Db	
476	LysGlnThrGlyGluSerAsnGluMetThrGlnLysAlaThrLysLeuGlyAlaG	457	Qy	
110	ATTATTGACCGACTCAAA	1083	Db	
456		437	Qy	
108	TTACAACATAATAACGCTGATTTGGCCTTGAACAAGGCAGACATGGCAGCGTTACAAAGT	1023	Db	
436	MetGlnGlnAsnVal	420	Qy	
102		978	Db	
419	AlaAlaProAlaLeu	404	Qy	
977	ACAAGTCGCCGTTGGTGTG	924	Db	
403	LysValIleSerSerLeuThrSerLysTrpValThrValGlyValGlyValValVal	385	Qy	
923		864	Дb	
384	IleSerLysValPheAlaLysGlyThrGlnMetIleAlaLysAsnPheProLysLeuSer	365	Qy	
863		804	фd	
364	Lе	353	Qy	
803		744	Дb	
352	AlaAlaIleLysAlaAlaValLysSerGlyIleLysAlaPheIleLysThr	336	Qy	
743	AGTTTCAACCGTAATGACC	684	рь	
335	ValleThrAlaValArgGlnAlaIleThr	326	Qy	
683	AATATGGCAGTGAAACAAGCGGCGGAAGATGGCCTGATATCCCCAAGAGGCAATGAAAATA	624	рь	
325	ValGlnAlaValValGlnAlaValLysGlnAla	315	Qy	
623	TCAGGGGTAGGAGCCGTTGCCGTGCAATGATGGTTGCCTCAGGCGTAATTGGGATGGCG	564	Db	
314		295	Qy	
563		504	рь	
294	AlaIlePheThrCysGlyAlaGlyLeuAlaGlyLeuAlaAlaGlyAlaAlaGlyAla	275	Qy	
503	AATGCCAAGCAAGTCAAGAAATCCGGCATCGCATC	468	Db	
274		255	Qy	
467	CATGAACAAAACATGAAGAAAATTGAAGAGAATCAAGAGAAAATCAAAGAAACAGAAGAG	408	Db	
254		235	Qy	
407	CTAGTTTCTAATTTAGAAGAAGTACGCAAAGACATAAAAATCGCTGATATTCAGCGTCTT	348	Вb	
234		220	Qy	
347	TCAGTGCTAACGAAGTTTACGCTTGCTTCACCTGATACATTTGAGATTGAGTTAGGTAAG	288	DЪ	

Best Local Similarity: 22.93% Mismatches: 206 Best Local Similarity: 6.54% Indels: 112 Query Match: 4.54% Gaps: 13  DB: US-09-889-314-2 (1-496) x US-09-103-840A-2 (1-4403765)  US-09-889-314-2 (1-496) x US-09-103-840A-2 (1-403765)  US-09-889-314-2 (1-403765) x US-09-103-840A-2 (1-403765)  US-09-889-314-2 (1-403765) x US-09-103-840A-2 (1-403765)  US-09-889-314-2 (1-403765) x US-09-103-840A-2 (1-403765)  US-09-889-314-2 (1-403	J3-840A-2/C J3-840A-2/C APPLICATION: AL INFORMATION: AL INFORMATION: ICANT: FLEISCHMAN, Robert D. ICANT: WHITE, Owen R. ICANT: WHITE, Owen R. ICANT: WHITE, Owen R. ICANT: VENTER, John C. E OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYS! E OF INVENTION: TUBERCULOSIS E OF INVENTION NUMBER: US/09/103,840A ENT FILING DATE: 1998-06-24 ENT FILING DATE: 1998-06-24 ERNT FILING DATE: 1998-06-24 IERN IMPORMATION Ver. 2.1 UNARE: PatentIn Ver. 2.1 WARE: PATENTIAN OF SEQUENCES INVERTIAN OF SEQUENCES INFORMATION: CDC 1551 IER INFORMATION: represent a, t, c or g 103-840A-2 INSTANCES: I.4 Length: Matches:	394 394 394
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Qy 480 TyralaalaileSerclyAlaileAlaGiyAla 490 [      :::::	
Oy 420 MetGlnGlnAsnValAlaGlnPheGlnLysGluValGlyLysLeuGlnALaAlaALAASP 439 11 ::	
Qy 400 GlyValValValAlaAlaProAlaLeuGlyLysGlyIleMetGlnMetGlnLeuSerGlu 419	
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Qy 360 AlaIleSerLysGlyIleSerLysValPheAlaLysGlyThrGInMeLLeALaLysGnyThrGInMeLLeALaLysGnyThrGInMeLLeALaLysGnyThrGInMeLLeALaLysGnyThrGInMeLLeALaLysGnyThrGInMeLLeALaLysGnyThrGInMeLLeALaLysGnyThrGInMeLLeALaLysGnyThrGInMeLLeALaLysGnyThrGInMeLLeALaLysGnyThrGInMeLLeALaLysGnyThrGInMeLLeALaLysGnyThrGInMeLLeALaLysGnyThrGInMeLLeAlaLysGnyThrGInMeLLeALaLysGnyThrGInMeLLeALaLysGnyThrGInMeLLeALaLysGnyThrGInMeLLeALaLysGnyThrGInMeLLeAlaLysGnyThrGInMeLleAlaLysGny	U 0
340 3937228	Qy Db
320 3937288	Qy Db
300 AlaAlaGlyAlaAlaAlaThrThrValAlaThrGlnIleThrValGlnAlaValVal	Qy
290 AlaAlaValGlyAlaAlaAlaAla	Qy dd
270 IleSerIleValAlaAlaIlePheThrCysGlyAlaGlyLeuAlaGlyLeuAlaAlaGly	Фр
250 GluGlyThrMetAspThrValAsnThrValMetLIteAldValSetValSetThrValAsnThrValMetLIteAldValSetValSetThrValSetThrValAsnThrValMetLIteAldValSetThrVa	Qy
3937481	Db
230 ₽	Qy
210 ThrGlnAlaGlnAlaAspGlnThrAsnLysLeuGlyLeuGluLysGlnAlaIleLysIle :::           :::	Qy Db
190 AlaLysAlaIleGlnThrLeuGlyGluAlaThrLysSerAlaLeuSerAsnTyrAlaSer 2 :::	Qy Db
176ValThrProArgSerGluVallleGluIleGlyLeuAlaLeu	Qу
-	Qy Db
3937777 GCCGTGGCCGCCGATGGCCCGTTGCCGCCATCGCCGCCGCCGCCGCCGTTGCCCGCCGGT 3937718	Db

Qy Db 3	Qy Db 3	Qy Db 3	Qу Db 3	Qy Db 3	Qy Db 3	US-0	Alignm Pred. Score: Percen Best I Query DB:	ý	ENZCOF	G	RESU US-0 ; Se	DЪ	ΩУ	B 3	) D	Qy	Ф	ν
154 3943555	139 }943615	94	943	943	59 3943780	09-889	nment . No.: e: ent S: Local y Mato		FILE REFERENCE: 24366-20007.00 CURRENT APPLICATION NUMBER: US/0 CURRENT FILING DATE: 1998-06-24 NUMBER OF SEQ ID NOS: 2 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 1 LENGTH: 4411529 TYPE: DNA	GENERAL INFORMATION: APPLICANT: FLEISCHA APPLICANT: WHITE; APPLICANT: FRASER, APPLICANT: VENTER, TITLE OF INVENTION:	SULT 27 -09-103-840 Sequence 1,	1052	364	992	935	324	875	309
->	ľΛ	MetGl	AspTh:	AlaPro	AlaTh	889-314-2	Score:       milar   Simi	INFOR	EFERENCE I APPLIC I FILING OF SEQ OF SEQ RE: Pate NO 1 H: 44115	INFORUNT: FINT: I	_ =	c 1052	у 364	CAGTG	TGCATO	nAlava	TGCGTO	1A1a
AlaAlaLeuSerGlyLysSerSerGlySerAlaLysLeuGluThr-         :::	SerLeuSerAlaAlaGlnMetLysGluValGlu- :::::     :::  GGAATTACGGTTGCCGCCGTTACCGCCATTGCC	nThrSe	rGlyVa CCGCTG	oGlnG1	rIleAl :::   CCGTTG	(1-496)	s: ity: larity	/cobac MATION	REFERENCE: 24366-20007.00 REFERENCE: 24366-20007.00 RIVER OF LISTON NUMBER: US/09 ENT FILING DATE: 1998-06-24 EN OF SEQ ID NOS: 2 RARE: Patentin Ver. 2.1 ONO 1 STH. 4411529 FINAL REFERENCE: DNA	RMATION: FLEISCHMAN, WHITE, Owe FRASER, C1 VENTION: DN VENTION: DN	1/c Applicat: 5294328	١٥		GTCAG	CAACCA	llleT	TGAGT	
rGlyLy ; cccrc	aAlaGI     TTGCCC	erileGl	lserG] ccccc <i>i</i>	nGlyVa        CCGGCC	aGlyAl         CCGGTG	6) x US-		terium : H37F	366-20 N NUME E: 19 OS: 2 Ver.	:  MAN, Robe Owen R.  Claire , Claire , John C : DNA SEC : TUBERC	ion			CCTCAG	GTGCGT	hrAlav	CAGCAT	
SSerS	nMetL: ::: CCGTT	LuGluA	LyAlaA      \GCGCC	IAlaA         STC	aSerG	-60	1.25 155.50 31.37% 23.25% 6.56%	tube:	007.00 BER: U: 998-06	Robert R. ire M. in C. SEQUE	us/09103			CAAGT	CAGCC	alArgo	CAACG	Thr
erGlys ;; ACCCTO	ysGluV ACCGCC	laSerL	laAlaT    GCCGGC	laGlyI       GCCGGC	lyLysa	103-84		rculos	0 S/09/1 -24		03840A			ACCAGT	CAGCA	GlnAla	AGTACG	SinIle
SerAla      CCCGC	/alGlu :: : :ATTGC	ysser	hrThr.      GCCAC	ysGlu GTCGC	spLys	0A-1	Length Matche Conser Mismat Indels Gaps:	is	03,84	FOR ST				GCTTC/	TCGAC	IleTh	TCAGC	ThrVa
CGGCCC	CACCTG	erMetGlu	AlaSer     CGTTAG	SerSer :::    CGCCAG	ThrSer	840A-1 (1-4411529	h: es: rvat rvat tche		OA	STRAIN ANALYSIS				AGCCTC	AAGCGC	cAlaAl	TCAGC	lGlnAl
GluTh:     CACCA	TGCCGG	SerTh	AsnTh	Gluse	SerTh	1529)	 6			NALYSI				HIII AGCGTO	CTC	aileLy	I AAGCAC	avalva
laAlaLeuSerGlyLysSerSerGlySerAlaLysLeuGluThr-ProGluLeuProLy       :::     :::	CGT	119 MetGlnThrSerIleGluGluAlaSerLysSerMetGluSerThrLeuGluSerLeuGln	99 AspThrGlyValSerGlyAlaAlaAlaThrThrAlaSerAsnThrAlaThrLysIleAla	79 AlaProGlnGlnGlyValAlaAlaGlyLysGluSerSerGluSerGlnLysAlaGlyAla	59 AlaThrIleAlaGlyAlaSerGlyLysAspLysThrSerSerThrThrLysThrGluThr     ::         780 GCCGCGTTGCCGGTGCC		441152 126 44 193 180 18			Ħ Z				CAGTGCGTCAGCCTCAGCAAGTACCAGTGCTTCAGCCTCAGCGTCGACAAGTGCGTCGGG	CAGCTTO	nalaVallleThralaValArgGlnalaIleThralaAlaIleLysAlaAlaValLysSe		ThrGlnIleThrValGlnAlaValValGlnAlaValLysGl
ProGluLeuProLy            GCCAGCGTTACCGC	Alavalvalval          GCCGCCGTCGCC	uSerLe ::::: GTGCCA	rLysIl     CCGTTG	sAlaGl        ccccc	sThrGl GTTG		9			MYCOBACTERIUM				GIGCGI	CAGCAA	laValL	CTTCTG:	lavalL
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173 39434	153 39435	138 : 39436	118 : 39436	98	78 39437					JM				1051	ف ۱	344	934	324
961	556	516	537	697	754													

Qy 434 uGlnAlaAlaAlaAspMetIleSerMetPheThrGlnPheTrpGlnGlnAlaSerLysIl 454
Db 3942553GGTACCTC 3942546
Qy 414 nMetGlnLeuSerGluMetGlnGlnAsnValAlaGlnPheGlnLysGluValGlyLysLe 434
Qy 394 pValThrValGlyValGlyValValValAlaAlaProAlaLeuGlyLysGlyIleMetG1 414 :::
Qy 381ProLysLeuSerLysVallleSerSerLeuThrSerLysTr 394
Qy 365 eSerLysValPheAlaLysGlyThrGlnMetIleAlaLysAsnPhe 380
Db 3942773 CCCCACCGTTGCTGCCAGCCGTGGCGGCCCCGGCAGCGCCGCCGTTGCCGCCGTCGCCGC 3942714
349 eIleLysThrLeuValLysAlaIleAlaLysAlaIleSerLysGly
Qy 332GINALAILETHTALAALAILELYSALAALAVALLYSSETGLYILELYSALAPH 349 :::   :::     Db 3942893 CGCCGTCCGCGCCGTTGCCGCCCTTGCCGCCGCCGCCGCC
Qy 317 aValVal GlnAlaValLysGlnAlaValIleThrAlaValArg 331
Qy 307
Qy 304 aAlaAla
Qy 288 aGlyAlaAlaValGlyAlaAlaAlaAlaGlyGlyAlaAlaGlyAlaAl 304
Qy 275
Qy 256 lAsnThrValMetIleAlaValSerValAlaIleThrValIleSerIleValAla 274
Qy 243 uGlnLysSerLysAspLeuGluGlyThrMetAspThrVa 256
Qy 223 uLysGlnAlaIleLysIleAspLysGluArgGluGluTyrGlnGluMetLysAlaAlaGl 243 Db 3943330
Qy 203 aLeuSerAsnTyrAlaSerThrGlnAlaGlnAlaAspGlnThrAsnLysLeuGlyLeuGl 223     :::    :::    :::
Oy 184 uIleGlyLeuAlaLeuAlaLysAlaIleGlnThrLeuGlyGluAlaThrLysSerAl 203
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US-08-961-527-773  Sequence 373, Application US/08961527  Patent No. 6420135  APPLICANT: Charles Kunsch APPLICANT: Charles Kunsch APPLICANT: Charles Kunsch APPLICANT: Charles Kunsch APPLICANT: Charles Kunsch APPLICANT: Charles Kunsch APPLICANT: Charles Sciences, Inc. STREER: 9410 Key West Avenue CITY: Rockville STRIE: Maryland COUNTRY: USA COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER READABLE FORM: SOFWARE: ASCII Text CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/961,527 FILING DATE: FILING DATE: FILING DATE: APPLICATION NUMBER: 35,373 REGISTRATION NUMBER: 53,373 REGISTRATION NUMBER: 53,373 REGISTRATION NUMBER: 9512  TELEPHNNE: (301) 309-8504 TELEPHNE: (301) 309-8504 TELEPHNE: (301) 309-8504 TELEPHNE: (301) 309-8512 INFORMATION FOR SEQ ID NO: 373: SEQUENCE CHARACTERISTICS: LENGTH: 1068 base pairs TYPE: nucleic acid STRANDENESS: double TOPOLOGY: Linear US-08-961-527-373	397 GGTTCAGCATCAACGAGTACGTCAGCTTCAGCGTCAACCAGTGCTTCAGCCTCAGCA 453 217 ThrasnLysLeuGlyLeuGluLysGlnAlaIleLysIleAspLysGluArgGluGluTyr 236 317 GLACAAGTGCGTCAGCCTCA

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Sequence 372, Application US/08961527
Patent No. 6420135
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INFUNITION: Streptococcus
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlyGluAlaThrLysSerAlaLeuSerAsnTyrAlaSerThrGlnAlaGlnAlaAspGln
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                                                                                                                                                                                                                                                            AlaValValGlnAlaValLysGlnAlaValIleThrAlaValArgGlnAlaIleThrAla 336
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DB:
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LENGTH: 807 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 424
PRIOR APPLICATION DATA:
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CITY: Rockville
STATE: Maryland
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE:
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TCAGCATCGACAAGTGCCTCGGCTTCAGCAAGCACATCAGCATCTGAATCAGCGTCAACC
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                                                                                                                                                           LeuGlnSerLeuSerAlaAlaGlnMetLysGluValGluAlaValValValAlaAlaLeu
                                                                                                                                                                                                                                                                                                        GlyAlaaspThrGlyValSerGlyAlaAlaAlaThrThrAlaSerAsnThrAlaThrLys 116
                                                                                                                                                                                                                                                                                                                                   AGTGCGTCACATTCAGCAAGTACCAGTGCTTCAGTCTCAGCATCAACAAGTGCTTCAGCC
                                                                                                                                                                                                                                                                                                                                                                                            TCAGCATCAACAAGTGCGTCGGCTTCAGCATCAACCAGTGCCTCCGGCTTCAGCGTCAACC
                                           ThrProArgSerGluValIleGluIleGlyLeuAlaLeuAlaLysAlaIleGlnThrLeu
                                                                                                   TCAGCTTCTGAATCGGCCTCA--
                                                                                                                           SerGlyLysSerSerGlySerAlaLysLeuGluThrProGluLeuProLysProGlyVal 176
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Indels:
Gaps:
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Conservative:
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DB:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENCTH: 941 base pairs
TYPE: nucleic acid
TYPE: nucleic double
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SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
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                                                                                                                                                                                                                                                                                                                                       AlaThrThrAlaSerAsnThrAlaThrLysIleAlaMetGlnThrSerIleGluGluAla 126
                                                                                                                                                                                                                                                                                                             TCAACGAGTGCATCAGCATCAGCATCAACGAGTGCATCGGCTTCAGCGTCAACCAGTGCA
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TCAGCAAGTACTAGTGCATCAGCATCAGCATCAACG---
                                                                                        LeuAlaLeuAlaLysAlaIleGlnThrLeuGlyGluAlaThrLysSerAlaLeuSerAsn 206
                                                                                                                                                    GluThrProGluLeuProLysProGlyValThrProArgSerGluValIleGluIleGly
                                                                                                                                                                                     AGTATCTCAGCGTCTGAATCGGCATCAACGAGTGCGTCAGCCTCAGCAAGTACTAGTGCA
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                           TyralaSerThrGlnAlaGlnAlaAspGlnThrAsnLysLeuGlyLeuGluLysGlnAla 226
                                                                                                                         TCGGCTTCAGCAAGCACCAGTGCGTCGGCTTCAGCATCAACCAGT--------
                                                            ---GCCTCAGCCTCAGCAAGTATCTCAGCGTCTGAATCGGCATCAACGAGTGCGTCAGCC 540
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Patent No. 6420135
GENERAL INFORMATION:
                                                                                                         US-08-961-527-370
Query Match:
                Percent Similarity:
Best Local Similarity:
                                                                            Alignment Scores:
                                                             Pred.
                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: MSDOS
SOFTWARE: ASCIT Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
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INFORMATION FOR SEO ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences NUMBER OF SEQUENCES: 391
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                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                           FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
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                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 36,373
                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                           TOPOLOGY:
                                                                                                                                                                       LENGTH:
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6.99%
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                                                       Length: Matches:
                                     Conservative:
                        Mismatches:
         Indels:
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US-08-961-527-263
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                                                                                 US-09-889-314-2 (1-496) x US-08-961-527-263 (1-3744)
                                                                                                                            Query Match:
                                                                                                                                          Best Local Similarity:
                                                                                                                                                                      Score:
                                                                                                                                                                                                                             US-08-961-527-263
                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                   Pred. No.:
                                                                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 263, Application US/08961527 Patent No. 6420135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                             TELEFAX: (301) 309-85
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12124
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                              2924 AGCACGACCAGTCAGTCACTTTCACAGTCTAAGTCACTCTCAGTAAGTGCTAGTCAA---
                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: MSDO
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                       LENGTH: 3744 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear
 44 IleGlnGlnThrArgGlnGlyLysAsnThrGluMetGluSerAspAlaThrIleAlaGly 63
                                                          24
                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                                                                                                                                                                                                                                           NAME: Brookes, A. Anders
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                     ThrSerThrProGlnGlyValProGlnGlnAspLysLeuSerGlyAsnGluThrLysGln 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTAACTCGACAGAGTGAAAGCTTAGGTGAGAGTGCGAAGCTCGAGCTGGATAAAGCGGCA 12125
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167.00
42.36%
22.22%
7.05%
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                                                                                                                                                                                                                                                                                                             263:
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                                                                                                                                                                    Length:
Matches:
                                                                                                                            Mismatches:
Indels:
                                                                                                                                                       Conservative:
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RESULT 23
US-08-961-527-368
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 368, Application Patent No. 6420135 GENERAL INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5
COMPUTER: HP Vectra 486/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2981
                                                                                                                                                                                                                                                                                                                               APPLICANT: Charles
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3524 CAAGCACCTCAGCTTCTGAATCGGCCTCAACCAGTGCGTCACCTCAGCATCGACAAGCGC 3583
                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3644 CAGTGCATCTGAATCGGCATCAACCAGTGCGTCAGCCTCAGCAAGTACTAGTGCATCGGC 3703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                303 aAlaAlaAlaThrThrValAla 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         263 ISerValAlaIleThrValIleSerIleValAlaAlaIlePheThrCysGlyAlaGlyLe 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               224 LysGlnAlaIleLysIleAspLysGluArgGluGluTyrGlnGluMetLysAlaAlaGlu 243
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                                                                                          COUNTRY: US
ZIP: 20850
                                                                                                                                                                             STREET: 9410 Ker
CITY: Rockville
                                                                                                                                                     STATE:
                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   uAlaGlyLeuAlaAlaGlyAlaAlaValGlyAlaAlaAlaAlaGlyGlyAlaAlaGlyAl 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GlnLysSerLysAspLeuGlu-GlyThrMetAspThrValAsnThrValMetIleAlaVa 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATCAACGAGTGCGTCTG-----AGTCAGCATCAACGAGTACGTCAGCCTCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGCACAAGCGCCTCGGGTTCAGCATCAACGAGTACGTCAGCTTCAGCGTCAACCAGTGCT 3418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAATCGGCCTCAACCAGCGCCTCGGCCTCAGCAAGCACCTCAGCTTCTGAATCGGCCTCA 3313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCTTCAGCAAGCACATCAGCATCTGAATCAGCGTCAACCAGTGCTTCGGCTTCAGCAAGT 319:
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                                                                                                                                                     Maryland
                                                                                                                                                                                                            9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                        Charles Kunsch
                                                                                                                         USA
                                                                                                                                                                                                                                            Human
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                                                                                                                                                                                                                                                                                                                               Streptococcus
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                               3.50
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                                  inch,
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                                  1.4Mb
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Percent Similarity:
Best Local Similarity:
Query Match:
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NAME: Seay, Nicholas J.

REGISTRATION NUMBER: 27386
REGISTRATION NUMBER: 960296.95017
REFERENCE/DOCKET NUMBER: 960296.95017
REFERENCE/DOCKET NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
TELECHANE: (608) 251-5000
TELECHANE: (608) 251-9166
INFORMATION FOR SEQ ID NO: 261:
SEQUENCE CHARACTERISTICS:
LENGTH: 45325 base pairs
TYPE: nucleic accid
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APPLICANT: Blattner, Frederick R.

Burland, Valerie

Perna, Nicole T.

Perna, Olcole T.
                                                                                                                                                                                                                                                                                 13546 GATATGAATGAGGCATCTAAAGCGTCAACCACGGCACAAAAGATGGCTAATCTTGTGGAT 13487
                                                                                                                                                                                                            13486 GCCAAAATTGCTGATGTTCAGAGTAGCACTGATAAGAATGCGAAAGCCAAACTTCCTCAA 13427
13306 GCGAATAACCTGACAACGGTAGTGAATAATAGCCAGCTCGAAATTCAGCAAATGTCGAAT 13247
                                                                       13426 GACGTGATTGACTATATAAACGATCCACGTAATGACATAAGTGTAACTGGTATTCGTGAT 13367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plunkett, Guy
Welch, Rod
TITLE OF INVENTION: No. 6365723el Sequences of E. coli 0157
NUMBER OF SEQUENCES: 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
COMPUTER: IBM PC compatible
OPERATING SUSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 8.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                               19 -----MetSerGlnValLeuThrSerThr-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 05/09/453,702B
FILING DATE: 03-Dec-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY, AGENT INFORMATION:
                                     39
                                                                                                                                                                            29 GlyVal-----
                                                                                                                                                                                                                                                                                                                  1 AspThrAsnMetSerIleSerSerSerSerGlyProAspAsnGlnLysAsnIle-----
                                                                                                          36 LeuSerGly----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID
                                 ---AsnGluThrLysGlnIleGlnGlnThrArgGlnGlyLysAsnThrGluMetGluSer 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Madison
STATE: WI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
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170.00
37.55%
21.19%
7.18%
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Matches:
Conservative:
Mismatches:
Indels:
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114
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208
128
23
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AG 12	
12403 TTATCTAAATTTGGTAATGTTGCTAACAAA	
TeLysThrLeuValLysAlaIleAlaLysAlaIleSerLysClyIleSerLysValPhe 369	2
	п ю
12523	D
314 ThrValGlnAlaVallVallySGlnAlaVallYSGlnAlaVellYSTHALAVeLAVelVSTH 12::: :::	ĸ
332	D
294 AlaAlaAlaAlaGlyGlyAlaAlaGlyAlaAlaA	Qy
12592 GCCGCTGTTTTTAACCCAGCACTCTGGGCTGTTGTTGCCALTGG	Db
274 AlaAlaIlePheThrCysGlyAla	νo
12643 AAAATTGTTGGCCAGGTCTTTGGTTGGGTGGGCGTCGCATTAACAGCCGTT 12	Db
254 AspThrvalAsnThrvalMetIleAlaValSerValAlaIleThrvalIleSerIleVal 2/3	QΥ
12703 CAGGAGTATAAAAAAACAGCTCGAAGAACAACAACAAGAAAGCCGAAGAAGAATCACAAAAAAAGT 12	ДD
234 GluGluTyrGlnGluMetLysAlaAlaGluGlnLysSerLysAspLeuGluGlyThrMet 2	γQ
12763 CTGAAAAACTCTAACGAGATTTATATGGATGGGCAAACTAAAGCGCTGGAGAATAAAACU	dd
214 A	Qy
12823 CAAATGATGATGATGGTCACTCTGTTATCCCTGGATACTTCCGCGCAGAAAGTCTCGAG	Db
194 GlnThrLeuGlyGluAlaThrLysSerAlaLeuSerAsnTyrAlaSerThrGlnAlaGln 213	Оу
12877 CCACAGCGCACAAGCTATCCCTATCTCTCAGGTGAATACCGTTGACCCTCAG 12	αα
174 proglyValThrProArgSerGluValIleGluIleGlyLeuAlaLeuAlaLysAlalle 193	Qy
12934 AGTAAATTGTTTGGTGGTATTAGTGGTGAGGTTACAAGTCGCACTGAGGAGGCAGAG 1	Db
euProLys 173	Qy
T 1233	Db
	Qy
A 12	Db
	QУ
CTGGTT	Db
ThrSerIleGluGluAlaSer	Qy
CCTCGGGTACTICIGGT 137	DЪ
	Qy
:::    6 TCAGCAATATCCCTTGGTAAATAACCGGAGATAACTATGCTTAACGTA 13	Db 5
78	2 5
13246 ACATTAAATCTCTTAACGAGTGCACGTTCTGATGTGCAATCTCTACAATATAGAACTATT 13187	글 5
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Percent Similarity:
Best Local Similarity:
Query Match:
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g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12584 GCCAAAATTGCTGATGTTCAGAGTAGCACTGATAAGAATGCGAAAGCCAAACTTCCTCAA 12525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12644 GATATGAATGAGGCATCTAAAGCGTCAACCACGGCACAAAAGATGGCTAATCTTGTGGAT 12585
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INFORMATION FOR SEQ ID NO: 206:
SEQUENCE CHARACTERISTICS:
LENGTH: 43360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12524 GACGTGATTGACTATATAAACGATCCACGTAATGACATAAGTGTAACTGGTATTCGTGAT 12465
  12134 AAATCCATGAACTCGTCAGCAGGCTGGACAGAAAGTAGCCCTTTACCGACGCCGCCGGCA 12075
                                                                              12179 ATTACTCAATCTGAAACGGGTTTATCGCTGGATTTACAA------CTGGTT 12135
                                                                                                                                                          12236 AATAACGATACCCTGTCTGTAACGTCTGGGGTTAATACC---GCCTCGGGTACTTCTGGT 12180
                                                                                                                                                                                                                                                                                                                      12344 ACATTAAATCTCTTAACGAGTGCACGTTCTGATGTGCAATCTCTACAATATAGAACTATT 12285
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                                     128 LysSerMetGluSerThrLeu----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29 GlyVal-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AspThrAsnMetSerIleSerSerSerSerGlyProAspAsnGlnLysAsnIle-----
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REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,702B
FILING DATE: 03-Dec-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                     AspAlaThrIleAlaGlyAlaSerGlyLysAspLysThrSerSerThrThrLysThrGlu 77
                                                                                                                 ThrThrAlaSerAsnThrAlaThrLysIleAlaMetGlnThrSerIleGluGluAlaSer 127
                                                                                                                                                                                                                                                                             ThrAlaProGlnGlnGlyValAlaAlaGlyLys------
                                                                                                                                                                                                                                                                                                                                                                                                GCGAATAACCTGACAACGGTAGTGAATAATAGCCAGCTCGAAATTCAGCAAATGTCGAAT 12345
                                                                                                                                                                                                                                                                                                                                                                                                                                   ---AsnGluThrLysGlnIleGlnGlnThrArgGlnGlyLysAsnThrGluMetGluSer 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTTAGTGGTGATTTAAGCGCTGGTGATCTGCAAACAGTGAAGGCGGCTATTTCAGCTAAA 12405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (608) 251-5000
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21.19%
7.18%
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RES US-	В	Qy	Qу	5	P &	Db	Qy	B 4	٥	В	Qy	Db	Qy	DЬ	Qy	Вb	Qy	db 44	} ;	P 6	5	3 2	٥	Qy Db	Ü	Qy	Ъ	Qy	DЪ	Qy	Db	Qy
ESULT 21 S-09-453-70 Sequence 2 Patent No.	11222	439	11282	11046	409	11384	389	Α.	370	11501	350	11561	333	11621	314	11645	294	11690	, i	254 11741		_	234	214 11861	17611	; <u>,</u>	11975	174	12032	154	12074	135
-702B-261/c e 261, Application US/09453702B No. 6365723	ĀG	AspMetIleSerMetPheThrGlnPheTrpGlnGlnAlaSerLysIleAlaSer 456	VALAIGI INPREGINELY SELLIVATED Y TOTAL AGENTAL AGENT A	ADIADA GOOGLI OUGANICI CERTI GILLIO I CICATA DE CONTROL CONTROL A CONTROL CONT	GlyLysGlyIleMetGlnMetGlnLeuSerGluMetGlnGlnAsn 423  GlyLysGlyIleMetGlnMetGlnLeuSerGluMetGln	ACGGTATTCGTT	ValValAlaAlaProAlaLeu 		AlaLvsGlvThrGlnMetIleAlaLvsAsnPheProLvsLeuSerLvsValIleSer 388	TTATCTAAATTTGGTAATGTTGCTAACAAAATTGGCTCAAGCGTTGTAAAAGTCGTT 1144	la	GGCGGAATATCTATGGCCGCAAGCATTCTGACAGCCGGCGTTGGCGGGGTGTCTTCACTG 1150	AlaIleThrAlaAlaIleLysAlaAlaValLysSerGlyIleLysAlaPhe 349	GCAGTCGATGTAATGGGGGAAAATGCCCCTCAGGGATTAAAGACTGCAGCACAGGTCTTT 1156	ThrValGlnAlaValValGlnAlaValLysGlnAlaValIleThrAlaValArgGln 332		AlaAlaAlaAlaGlyGlyAlaAlaGlyAlaAlaAlaAlaThrThrValAlaThrGlnIle 313	GCCGCTGTTTTAACCCAGCACTCTGGGCTGTTGTTGCCATTGGT 1164	alaglvalaglvienalaglvienalaglvalaglvalavalglv 293	AspThrValAsnThrValMetileAlaValSerValalaiLeThVValIleSerIleVal 2/3	ا ا ا	:::::::	GluGluTvrGlnGluMetLvsAlaAlaGluGlnLysSerLvsAspLeuGluGlyThrMet 253	AlaaspGlnThrAsniysLeuGlyLeuGluLysGlnAlaILeLysILeAspLysGluArg 233 AlaaspGlnThrAsniysLeuGlyLeuGluLysGlnAlaILeLysILeAspLysGluArg 233 CTGAAAAACTCTAACGAGATTTATATGGATGGGCAAACTAAAGCGCTGGAGAAATAAAACG 1180	AAATGATGATGGTCACTCTGTTATCCCTGGATACTTCCGCGCAGAAAAGTCTCGAGT	GlnThrLeuGlyGluAlaThrLySSerAlaLeuSerAsnTyrAlaSerThrGlnAlaGln 213	CACAGCGCACAAGCTATCCCTATCTCTCAGGTGAATACCGTTGACCCTCAG	laile 193	AGTAAATTGTTTGGTGGTATTAGTGGTGAGGTTACAAGTCGCACTGAGGAGGCAGAG 1197	AlaAlaLeuSerGlyLysSerSerGlySerAlaLysLeuGluThrProGluLeuProLys 173	GGTCACTCATTAGTGACGCCCTCTGCTGCTGAGGATGTCCTT 1203	GluSerLeuGlnSerLeuSerAlaAlaGlnMetLysGluValGluAlaValValVal 153
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1492 AGTGTTAACTCTGCCACACACAGGG---GGAGGAAGTGTCGCTTCTGCT 1536

475 GlnIleLeuLysAlaTyrAlaAlaIleSerGlyAlaIleAlaGlyAla 490

ThrGlnLysAlaThrLysLeuGlyAla 474

RESULT 19 US-08-961-527-369

Sequence 369, Application US/08961527 Patent No. 6420135 GENERAL INFORMATION:

APPLICANT: Charles Kunsch TITLE OF INVENTION: Strept NUMBER OF SEQUENCES: 391 CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland

COUNTRY:

USA

20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb
MEDIUM TYPE: Diskette 486/33
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527

CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

FILING DATE:

double  double  2.34e-08	FORM: Iskette, 3.50 inch, 1.4Mb storage sctra 486/33 4: MSDOS version 6.2 I Text DN DATA: BER: US/08/961,527  424 DATA: BER: BER: BER: US/08/961,527  1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	TRATGCTGTTGCCAGATTAAATAAATTTCTTGGTGCAGCGGGTGAT 1431  TRATGCTGTTGCCAGATTAAATAAATTTTCTTGGTGCAGCGGGTGAT 1431  LACAAATTATTTCCACCCATTTAAACCAAGCAGTTTTATTTA
RESULT 20 US-09-453-702B-206/c US-09-453-702B-206/c ; Sequence 206, Application US/09453702B ; Sequence 206, Application US/09453702B ; Sequence 206, Application US/09453702B ; Sequence 206, Application US/09453702B ; Sequence 206, Application US/09453702B ; Patent No. 6365723cl Sequences of E. coli O157  ITILE OF INVENTION: NO. 6365723cl Sequences of E. coli O157  NUMBER OF SEQUENCES: 265 CORRESPONDENCE ADDRESS: ADDRESSEE: Quarles & Brady STREET: 1 South pinckney Street CITY: Madison STATE: WI COUNTRY: US ZIP: 53701-2113 COMPUTER READABLE FORM: MEDIUM TYPE: DISKETLE, 3.50 inch. 1.44Mb storage OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Word Perfect 8.0	Qy 233ArgGluGluTyrGlnGluMetLysAlaAlaGluGlnLysSerlysAspLeuglug	Qy 118 AlaMetGlnThrSerIle

APPLICALLE
FILING DATE:
FILING DATE:
FILING DATE:
FILING DATE:
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
ANABE: BrOOKES, A. Anders
REGISTRATION UNMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8512
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 369:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 869 base pairs
LENGTH: 869 base pairs

Query Match: DB:

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> 66 79

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99 AspThrGlyValSerGlyAlaAlaAlaThrThrAlaSerAsnThrAla---ThrLysIle 117

TCAGAGTCAGCAAGTACCAGTGCGTCAGCTTCCGCATCAACAAGTGCCTCGGCTTCAGCA 125

Percent Similarity:
Best Local Similarity:

US-09-889-314-2 (1-496) x US-08-961-527-369 (1-869)

59 AlaThrIleAlaGlyAlaSerGlyLysAspLysThrSerSerThrThrLysThrGluThr 78

AGTACTAGTGCATCAGCTTCAGCATCAACGAGTGCATCGGCTTCTGCGTCAACCAGTGCA 65 AlaProGlnGlnGlyValAlaAlaGlyLysGluSerSerGluSerGlnLysAlaGlyAla 98

US-08-961-527-369

TYPE: nucleic acid STRANDEDNESS: doub TOPOLOGY: linear

Alignment Scores:

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Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-591-079-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECAMUNICATION INFORMATION:
TELEPHONE: (202) 887-0764
TELEFAX: (202) 887-0764
TELEFAX: 40-4030 MRSUNFOERSWSH
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENUTH: 1743 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: misc_feature
LOCATION: 1.1743
OTHER INFORMATION: /note= "Shigella flexneri ipaB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Livrat, Shuuel
REGISTRATION NUMBER: 33,949
REFERENCE/DOCKET NUMBER: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Apoptosis Induced by Shigella Ipab
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Zychlinksky, Arturo APPLICANT: Chen, Yajing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                              496
                                                                                                                  436 AACGCAGATTCTAAAATAAAAGACCTAGAAAATAAAATTAACCAAATTCAAACAAGATTA 495
                                                                                                                                                                                         376 CTTCTATCTGAAACTGAAGGACTAACCAGAGACTATGAAAAACAAATTAATAAACTAAAA 435
                                                                                                                                                                                                                                                            316 AAGTCCCAGCAACAGGCAAGACAGCAAAAAAACCTAGAATTCTCCGATAAAATTAACACT 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
LOCATION:
                                                               76 ThrGluThrAlaProGlnGlnGlyValAlaAlaGlyLysGluSerSerGluSerGlnLys 95 :::
                                                                                                                                                                                                                            55
                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 2000 Penr
CITY: Washington
STATE: DC
           96 AlaGlyAlaAspThrGlyValSerGlyAlaAlaAlaThrThrAlaSerAsnThrAlaThr 115
                                                                                                                                                    56 GluSerAspAlaThrIleAlaGlyAlaSerGlyLysAspLysThrSerSerThrThrLys 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/591,079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: MORRISON & FULLY STREET: 2000 Pennsylvania Avenue, NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
                                              TCGAACCTCGATCCA----
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185.00
38.10%
21.17%
7.81%
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                                            ----GAGTCACCAGAAAAGAAAAA 531
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105
84
171
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465	SerLysIleAlaSerLysGlnThrGlyGluSerAsnGluMet	452	Qy
1371	ATAGGTAAAACCCTCACAGACCTTATACCAAAGTTTCTCAAGAATTTTTCTTCTCAACTG	1312	Db
451	nAlaAlaAlaAspMetIleSerMetPheThrGlnPheTrpGlnG	435	Qy
i		1273	Db
434	MetGlnLeuSerGluMetGlnGlnAsnValAlaGlnPheGlnLysGluValGlyLysLe	415	Qy
N		w	DB 43
41	. ValuhrvalcivvalcivvalvalvalvalalabiaDroalaioncivv.vccivTleMetCin	202	Q
1230	AGCCAAAATGATTGGCTCTATTCTGGGGGCAATCGCAGGCGCTCT	1171	Дb
394	MetIleAlaLysAsnPheProLysLeuSerLysValIleSerSerLeuThrSerLysTrp	375	Qy
1170	AAACTCCTTTCAGATGCATTTACAAAAATGCTCGAAGGCTTGGGC	1126	Db
374	/sAlaIleSerLysGlyIleSerLysVal	355	Qy
1125	AATTCCTTCATGGAACAAGCCCTGAATCCGATCATGAAAGCAGTCATTGAAACCCTTAATC	1066	Db
354	heIleLysThrLeuVa	335	Qy
1065	ACGGATGCTATAGTACAAGCAGCGACCGGC	1036	Db
334	ValGlnAlaValValGlnAlaValLysGlnAlaValIleThrAlaValArgGlnAlaIle	315	Qy
1035	ATGGTT	1030	Db
314	AlaAlaAlaGlyGlyAlaAlaGlyAlaAlaAlaAlaThrThrValAlaThrGlnIleThr	295	Qy
1029	GCAGCTTTTTCTGGAGGAGCCTCTCTAGCACTGGCAGCTGTTGGTTTAGCTCTT	976	Dъ
294	laIlePheThrCysGlyAlaGlyLeuAlaGlyLeuAlaAlaGlyAlaA.	275	Qy
975	TGTGTTGGGGAAAATACTTGGGGCACTTTTAACTATCGTTAGTGTTGCA	925	рь
274	etIleAlaValSerValAlaIleThrValIleSerIleValAl	255	Qy
924	TAT	877	Дb
254	yrGlnGluMetLysAlaAlaGluGlnLysSerLysAspLeuGl	236	Qy
876	GAATCAAGAAAAACTGAAATGGAGAGAAAATCTGATGAG	838	Db
235	lnThrAsnLysLeuGlyLeuGluLysGlnAlaIleLysIleAspLysGluArg	216	Qy
837	AATCTTTAAAAAATGATCTGGC	778	DЬ
215	rAlas	196	Qy
777	TTTATT	736	Db
195	alThrProArgSerGluValIleGluIleGlyLeuAlaLeuAlaL	176	Qy
735	AAACACAGCATCTGCTGAACAGCTATCAACCCAGCAGAAATCATTAA	679	Db
175	GlyLysSerSerGlySerAlaLysLeuGluThrProGluLeuProLysPro	156	Qy
678	AAACTTACAGATAAATCAATGCAACTCGAAAAAGAAATAGACTCTTTTTCTGCA	625	Db
155	SerLeuGlnSerLeuSerAlaAlaGlnMetLysGluValGluAlaValValValAlaAla	136	Qy
624	AAAGACAGGACATTGATTGAGCAGAAAACCCTGTCAATTCATAGC	580	Db
135	IleAlaMetGlnThrSer	116	Qy
579	TTAAGCCGGGAAGAAATACAACTCACTATCAAAAAAAGACGCAGCAGTT	532	Db

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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FEATURE:
NAME/YEY: modified_base
LOCATION: (127)
OTHER INFORMATION: R = A OR G
US-09-125-619-3
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SEQ ID NO 3
LENGTH: 77
TYPE: DNA
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APPLICANT:
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TITLE OF INVENTION: VMP-LIKE SEQUENCES OF PATHOGENIC BORRELIA
FILE REFERENCE: UTSH:234
CUGREENT APPLICATION NUMBER: US/09/125,619
CURRENT FILING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52 GCTGTTAGTGCTGTTAGTGGG-------GAGCAGATATTAAGTGCGATTGTTAAG
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                                                                                                                                                                                                                 394
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175 GlyValThrProArgSerGluValIleGluIleGlyLeuAlaLeuAlaLysAlaIleGln 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SerThrProGlnGlyValProGlnGlnAspLysLeuSerGlyAsnGluThrLysGlnIle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTGCTGCTGCTATTGGGAAGGGTAATGAGGATGGTGCGGAGTTTAAGGATGAGATGAAG 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GlnGlnThrArgGlnGlyLysAsnThr------GluMetGlu 56
                                                                                                                                                                                                                                                                                                                                                                   SerThrThrLysThrGluThrAlaProGlnGlnGlyVal-----AlaAlaGlyLysGlu
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                                                                                                                  AlaAlaGlnMetLysGlu-----
                                                                                                                                                                                  GluAlaSerLysSerMetGluSerThrLeuGluSerLeu-----GlnSerLeuSer 141
                                                                                                                                                                                                                 ATTGGAGAAGTTGTGGCTGATGATAATGCTGCGAAGGTTGCTGATAAGGCGAGTGTGAAG 453
                                                                                                                                                                                                                                                                            TTGGATAAGCTGGTAAAAGCTGTAAAGACAGCTGAGGGGGCTTCAAGTGGTACTGCTGCA 393
                                                                                                                                                                                                                                                                                                        SerSerGluSerGlnLysAla-------GlyAlaAspThrGlyValSerGly 104
                                                                                                                                                                                                                                                                                                                                      GCTGTGAAAATGATGAGAAAGGGAAGGCTGAGGGGGCTATTAAGGGAGCTGGCGAGTTG 333
                                                                                                                                                                                                                                            AlaAlaAlaThrThrAlaSerAsnThrAlaThrLysIleAlaMetGlnThrSerIleGlu 124
                             GCTCATGCTGGGGACAGTGAGGCTGCTAGCAAG----
                                                 AlaLeuSerGlyLysSerSerGlySerAlaLysLeuGluThrProGluLeuProLysPro 174
                                                                                          GTTGCTGCTGAAAGAGGGCAATGAAAAGGCAGGGAAGTTGTTTGGGAAAGTTGATGCT
                                                                                                                                                     GGGATTGCTAAGGGGATAAAGGAGATTGTTGAAGCTGCTGGGGGGGAGTAAAAAGCTGAAA 513
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HARDHAM, JOHN M.
HOWELL, JERRILYN K.
BARBOUR, ALAN G.
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186.00
37.00%
23.29%
7.85%
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Indels:
Gaps:
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Matches:
Conservative:
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US	ρb	ОУ	Qy Db	Db	Qy	Дb	Qy	dd dd	Oy	Db .	0у	ρb	Oy	рb	Qy	рb	Qy	Db	Qy	Db 43	Q !	Db :	Qγ	Db	Qy	Db :	Qy	Db	QY	рь	Qy	Db	Qy	Db
RESULT 18 US-08-591-079-1	1501 CTGGTAAAAGCTGTAAAGACAGCTGAGGGGGCTTCAAGTGGT 1342	478LysalaTyralaalaIleSerGlyalaIleAlaGly 489		477	PheThrGlnPheTrpGlnGlnAlaSerLysIleAlaSerLySGlnTnI 4	150	sp 43	GCTACAAATCCGATTGCTGCTATTGGGAAGGGT1	AlaProAlaLeuGlyLySGlyIleMetGlnMetGlnLeuSerGlu 41	HI HI HI HI HI HI HI HI HI HI HI HI HI H		77 AGTGAGGCTGGTAGCAAGGCGGCTGGTGGTGAGTGCTGTTAGTGGGGAGCAGATATTA	PheProLysLeuSerLysValIleSerSerLeuThrSerLysTrpValThr	, t	361 IleSerLysGlyIleSerLysValPheAlaLysGlyThrGlnMetIleAlaLySAS0 3/5		aValLysSerGlyIleLysAlaPhe			52 GGGGCTTCAAGTGGTACTGATGCAATTGGAGAAGTTGTGGCTAATGCTGGTGCTGCAAAG	2	 			SerTleValAlaAlaIlePheThrCysGlyAlaGlyLeuAlaGlyLeuAlaGlyLeuAlaGly	99CAGATTGCTGCTGCTATTGCTTGAGGGGGATG	<pre>;51 GlyThrMetAspThrValAsnThrValMetIleAlaValSerValAlaIleThrValIle ;;; ;;       ;;; ;;     ;;; ;;   ;;; ;;</pre>		euGl				95 ThrLeuGlyGluAlaThrLysSerAlaLeuSerAsnTyrAlaSerThrGlnAlaGln	607GCGGCTGGTGCTGTTAGT 624

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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                         Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 365
SEQUENCE CHARACTERISTICS:
LENGTH: 1436 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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TITLE OF INVENTION: Strep
NUMBER OF SEQUENCES: 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
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   358 GCTTCAGCATCAACA-----AGTGCTTCAGCTTCAGCAAGTATCTCAGCGTCTGAATCG 411
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CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid STRANDEDNESS: doub
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                          22 ValLeuThrSerThrProGlnGlyValProGlnGlnAspLysLeuSerGlyAsnGluThr 41
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                                                                                                       2 ThrAsnMetSerIleSerSerSerGlyProAspAsnGlnLysAsnIleMetSerGln 21
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                                                                       ACAAGTGCGTCGGCTTCAGCAAGTACCTCAGCGTCTGAATCAGCATCAACGAGTGCATCA 357
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188.00
37.30%
21.35%
7.94%
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Matches:
Conservative:
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Indels:
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79
59
214
18
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eIleLysThrLeuValLysAlaIleAla 358             aGCATCAACCAGTGCTTCGGCTTCGGCA 1392	349 PheIleLysThr       1363 TCAGCATCAACC	Db Qy
AlaValArgGlnAlaIleThrAlaAlaIleLysAlaAlaValLysSerGlyIleLysAla 348               :::       :::                :::       ::: 	329 AlaValArgGln     1306 GCCTCGGCTTCA	Qy Db :
alAlaThrGlnIleThrValGlnAlaValValGlnAlaValLysGlnAlaValIleThr 328	309 ValAlaThrGln :::      1246 GCATCAACCAGT	Qy Db
lyAlaAlaValGlyAlaAlaAlaGlyGlyAlaAlaGlyAlaAlaAlaAlaThrThr 308	289 GlyAlaAlaVal :::    1186 GCGTCAGCTTCC	Qy Db :
ValIleSerIleValAlaAlaIlePheThrCysGlyAlaGlyLeuAlaGlyLeuAlaAla 288 :::	269 ValIleSerIle ::: 1126 GCATCAACGAGT	Db :
LeuGluGlyThrMetAspThrValAsnThrValMetIleAlaValSerValAlaIlleThr 268 :::       :::       :::         :::	249 LeuGluGlyThr ::: 1066 GCCTCGGCTTCA	Qy Db
IleAspLysGluArgGluGluTyrGlnGluMetLysAlaAlaGluGlnLysSerLysAsp 248    :::       :::       :::       :::      :::	229 IleAspLysGlu 1006 GCATCAACGAGT	Qy Db 1
AlaGlnAlaAspGlnThrAsnLysLeuGlyLeuGluLysGlnAlaIleLys 228	212 AlaGlnAlaAsp           946 GCATCAGCTTCA	Qy
AlaIleGlnThrLeuGlyGluAlaThrLysSerAlaLeuSerAsnTyrAlaSerThrGln 211 	192 AlaIleGlnThr     ::: 886 GCAAGTACCTCA	Qу
roLysProGlyValThrProArgSerGluValIleGluIleGlyLeuAlaLeuAlaLys 191 ::: ::: CTTCAGCAAGTACCAGTGCGTCAGCCTCAGCGTCGACAAGTGCGTCGGCTTCA 885	172 ProLysProGly 832 GCTTCAGCAAGT	Qy Db
ValValAlaAlaLeuSerGlyLysSerSerGlySerAlaLysLeuGluThrProGluLeu 171 	152 ValvalAlaAla     :::  772 ACTAGTGCATCA	Qу
SerThrLeuGluSerLeuGlnSerLeuSerAlaAlaGlnMetLysGluValGluAlaVal 151 :::::	132 SerThrLeuGlu :::::: 712 GCCTCAGCAAGT	Qy Db
ThrLysIleAlaMetGlnThrSerIleGluGluAlaSerLysSerMetGlu 131 	115ThrLys     652 GCGTCGACAAGT	Qy Db
ValSerGlyAlaAlaAlaThrThrAlaSerAsnThrAla	102 ValSerGlyAla.     ::: 592 GCCTCAGCTTCA	Qу
GlnGlyValAlaAlaGlyLysGluSerSerGluSerGlnLysAlaGlyAlaAspThrGly 101	82 GlnGlyValala: ::: 532 GCAAGCACATCA	Qy Db
AlaGlyAlaSerGlyLysAspLysThrSerSerThrThrLysThrGluThrAlaProGln 81	62 AlaGlyAlaSer(	Qy Db
LysGlnIleGlnGlnThrArgGlnGlyLysAsnThrGluMetGluSerAspAlaThrIle 61 :::     :::    GCATCAACGAGTGCGTCCGCTTCAGCAAGTACTAGCGCCTCAGCATCAGCGTCAACAAGT 471	42 LysGlnIleGln	Qy Db

RESULT 17 US-09-125-619-3 Sequence 3, Application US/09125619 Patent No. 6437116

GENERAL INFORMATION:

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US-08-961-527-364
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Patent No. 6420135
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Best Local Similarity:
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OPERATING SYSTEM: MSDOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (301) 309-8504
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 364:
SEQUENCE CHARACTERISTICS:
LENGTH: 2550 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
COMPUTER: HP Vectra 486/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Charles Kunsch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Marvi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            No . .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 20850
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                                                                                                                                                                                                                               349 TCAGCCTCAGCGTCGACAAGTGCGTCGGCCTCAACCAGTGCATCTGAATCGGCATCAACC 408
                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
                                                                                                                                                                      409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                   105
                                                                                                            469
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                                                                                                                                                                                                45 GlnGlnThrArgGlnGlyLysAsnThrGluMetGluSerAspAlaThrIleAlaGlyAla 64
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                                                                                                                                                                                                                                                                                                                    SerIleSerSerSerSerGlyProAspAsnGlnLysAsnIleMetSerGlnValLeuThr
AlaalaalaThrThrAlaSerAsnThrAla---ThrLysIlealaMetGlnThrSerIle 123
                                                                                                                                                                                                                                                          SerThrProGlnGlyValProGlnGlnAspLysLeuSerGlyAsnGluThrLysGlnIle 44
                                              AGTGCTTCAGTCTCAGCATCAACAAGTGCTTCAGCCTCAGCATCGACAAGTGCCTCGGCT 588
                                                                                                          TCAGCATCAACCAGTGCCTCGGCTTCAGCGTCAACCAGTGCGTCAGCTTCAGCAAGTACC 528
                                                                                                                                    SerGlyLysAspLysThrSerSerThrThrLysThrGluThrAlaProGlnGlnGlyVal 84
                                                                                                                                                                    AGTGCGTCAGCCTCAGCAAGTACTAGTGCATCAGCTTCAGCATCAACGAGTGCATCGGCT 468
                                                                        AlaAlaGlyLysGluSerSerGluSerGlnLysAlaGlyAlaAspThrGlyValSerGly 104
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192.00
33.97%
20.99%
8.10%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MSDOS version 6.2
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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110
68
275
71
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GTCACTTCC	1597 GTGCATCAGAGTCAGCAAGT	В
AlaAs	430GluValGlyLysI	Qy
CTTCAGCATCAACGAGTGCATCGGCTTCGGCGTCAACCA	1537 CAGCAAGTACTAGTGCATCAG	Dр
	1 1 1	Qy
AACCAGTGCATCTGAATCGGCATCAACCAGTGCGTCAGCT	::::::::: 1477 TCGACAAGTGCGTCGGCCTC	Dp -
GlnAsnValAlaGlnPh	417 uSerGluMetGln	Οy
	1417 TCAGCTTCAGCAAGTACCAG	σb
GlyValGlyValValValAlaAlaProAlaLeuGlyLys-GlyIleMetGlnMetGlnLe 417	398 GlyvalGlyvalvalvalAl	QУ
	1357 AGCACATCAGCTTCTGAATC	ф
	378 LysAs	Qy
	358 AlaLysalalleSerLysel                    1306 GCGTCAACGAG	DP QA
	TCCGCTT	Db
leLysAlaAlaValLysSerGlyIleLysAlaPheIleLysThrLeuValLysAlaILe 35/	338 IleLysAlaAlaValLysSei     :::	Qy
	1189 AGCACAAGTGCTTCAGCCTCA	Dр
. ~	318 ValValGlnAlaValLysGlr	Qy
, –	29 TCTGA	Db :
nAla 317 	298 GlyGlyAlaAlaGlyAlaAla	Qy
	1069 TCAACCAGTGCTTCAGCCTCA	Db :
		QV !
	09	로 :
		Qy
AGCACCTCAGCTTCTGAATCGGCCTCAACCAGCGCCTCAGCCTCAGCATCAACGAGTGCT 1008	949 AGCACCTCAGCTTCTGAATCG	Db
	243 GluGlnLysSerLysAspLeu	Qy
TCAGCA 9	889 TCGGCCTCAGCAAGCACCTCAG	Db
	223 GluLysGlnAlaIleLysIleA	Qy
AGCGCC	835 AGTGCTTCGGCTTCAGCAAGTA	Db
	203 AlaLeuSerAsnTyrAlaSerT	Qγ
ATCTGAATCAGCGTCAACC 8	790	Db
IleGluIleGlyLeuAlaLeuAlaLysAlaIleGlnThrLeuGlyGluAlaThrLysSer 202	183 IleGluIleGlyLeuAlaLeuA	Qy
		pb -
luThrProGluLeuProLysProGlyValThrProArgSerGluVal 182	63	ον !
::: TCAACGAGTGCATCGGCTTCGGCGTCAACCAGTGCATCAGAGTCAGCAAGTACCAGTGCG 768		궁 5
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rlysSerMetGluSerThrLeuGluSerLeuGlnSerLeuSerAla 142	2 0	}
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1702 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA: APPLICATION NUMBER:
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617
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STREET: 9410 Key
CITY: Rockville
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 424
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                                                                                                                                                                                                                                                                                    59 AlaThrIleAlaGlyAlaSerGlyLysAspLysThrSerSerThrThrLysThrGluThr 78
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                                                                                                                                                                                                                    AlaProGlnGlnGlyValAlaAlaGlyLysGluSerSerGluSerGlnLysAlaGlyAla 98
                                                                                                                                                                                                                                                                                                                                                                 AsnGluThrLysGlnIleGlnGlnThrArgGlnGlyLysAsnThrGluMetGluSerAsp 58
                                                                                                                                                              AspThrGlyValSerGlyAlaAlaAlaThrThrAlaSerAsnThrAla------ 114
                                                                                                                                                                                                 TCGGCTTCAGCATCAACCAGTGCATCAGAGTCAGCAAGTACCAGTGCGTCAGCTTCCGCA 496
                                                                                                                                                                                                                                                                   TCAACCAGTGCGTCAGCCTCAGCAAGTACTAGTGCATCAGCCTTCAGCATCAACGAGTGCA 436
SerLysSerMetGluSerThrLeuGluSerLeuGlnSerLeuSerAlaAlaGlnMetLys 146
                                                                TCAGCTTCCGCGTCAACCAGCGCCTCGGCCTCAGCAAGTATCTCAGCGTCTGAATCGGCA
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9410 Key West Avenue
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Indels:
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	GAGTGCGTCAGCCTCAGCAAGCACATCAGCTTCTGAAT 1685	1648	DЪ
	eSerGlyAlaIleAlaGly-AlaHisLysThrAsnAsn 495	483	Qy
1647	TTCAGCATCGACAAGTGCGTCTGAATCGGCATCAACGAGTGCTTCGGCTTCAGCATCAAC	1588	Db
483	rAlaAl	463	Qy
1587	AAGTGCCTCGGCTTCAGCAAGCACCAGTGCGTCGGCTTCAGCAAGTACTAGTGCATCGGC	1528	Db
463	tPheThrGlnPheTrpGlnGlnAlaSerLysIleAlaSerLysGlnThrGlyGluSerAs	443	Оу
1527	TTCAGCATCAACGAGTGCTTCAGTCTCAGCGTCAACCAGTGCCTCTGAATCAGCATCAAC	1468	망
443	tileSerMe	423	Qy
1467	GAGTGCATCAGCTTCAGCATCAACAAGTGCTTCAGCTTCAGCAAGTACCAGTGCGTCGGC	1408	Db
423	aProAlaLeuGlyLysGlyIleMetGlnMetGlnLeuSerGluMetGlnGlnAs	403	Qy
1407	CTCAGCGTCGACAAGTGCGTCGGCTTCAGCAAGTACCTCAGCGTCTGAATCAGCATCAAC	1348	Db
403		383	Qy
1347	.AGC	1297	Db
383	sGlyIleSerLysValPheAlaLysGlyThrGlnMetIleAlaLysAsnPheProLysLe	363	Qy
1296	TACCAGCGCCTCAGCTTCAGCAAGCACCAGTGCGTCAGCCTCAGCAAGTACCAGCGCCTC	1237	Дb
363		343	Qy
1236	TTCAGCAAGTACTAGTGCATCAGCATCAGCATCAACGAGTGCATCGGCTTCAGCAAG	1180	Db
343		323	Qy
1179	AGCCTCAGCAAGTACTAGCGCCTCAGCCTCAGCATCAACGAGTGCGTCCGC	1129	Db
323	lnIleThrValGlnAlaValValGlnAlaValLy	303	Qy
1128	AGCGTCGACAAGTGCGTCGGCCTCAACCAGTGCATCTGAATCGGCATCAACCAGTGCGTC	1069	Db
303		283	Qу
1068	CAGCAAGTACCAGTGCTTCAGCCTC	1030	Db
283	erValAlaIleThrValIleSerIleValAlaAlaIlePheThrCysGlyAlaGlyLe	263	Qy
1029	ACCAGTGCGTCAGCCTCAGCATCGACAAGCGCCTCAGCTTCAGCAAGTAC	970	Db
263	uGlnLysSerLysAspLeuGluGlyThrMetAspThrValAsnThrValMetTleAlaVa ::: ::: :::	243	Qy
969	AGTGCGTCTGAGTCAGCATCAACGAGTACGTCAGCCTCAGCAAGC-ACATCAGCTTCTGA	911	Вb
243	uMetLysAlaAlaGl	226	Qy
910	TCAGCAAGTACTAGCGCCTCAGCATCAGCGTCAACAAGTGCTTCGGCTTCAGCGTCAACG	851	DЪ
226		207	Qy
850	AGTGCTTCAGCCTCAGCAAGTATCTCAGCGTCTGAATCGGCATCAACGAGTGCGTCCGCT	791	Дb
206		187	Qy
790	AGTACCTCAGCATCTGAATCAGCATCAACAAGTGCATCGGCTTCAGCAAGCA	737	Дb
186	IleGly	167	Qy
736	TCGGCCTCAGCAACCAGCGCGTCTGAATCCGCATCAACCAGTGCCTCAGCTTCAGCA	677	Db
166		147	Qy

COUNTRY:

20850

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Query
DB:
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Best Local Similarity:
Query Match:
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER PB:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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NAME: Brookes, A. Anders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 4483 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                749
                                                                                                                                                                                                                                                                                                       62 AlaGlyAlaSerGlyLysAspLysThrSerSerThrThrLysThrGluThrAlaProGln
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                                                                                                                                                                                                                                                                                                                                   GCTTCGGCGTCAACC------
                                                                                                                                                                                                                                                                                                                                                                                                                         ValLeuThrSerThrProGlnGlyValProGlnGlnAspLysLeuSerGlyAsnGluThr
                                                                                                                                                            ValSerGlyAlaAlaAlaThrThrAlaSerAsnThrAlaThrLysIleAlaMetGlnThr 121
                                                                                                                                                                                                                    GCAAGTATCTCAGCGTCTGAATCGGCATCAACGAGTGCGTCCGCTTCAGCAAGTACTAGC
                                                                                                                                                                                                                                             GlnGlyValAlaAlaGlyLysGluSerSerGluSerGlnLysAlaGlyAlaAspThrGly 101
                                                                                                                                                                                                                                                                              GCGTCGGCTTCAGCAAGTACTAGCGCCTCAGCCTCAGCCTCAACCAGTGCGTCAGCCTCA 898
GlySerAlaLysLeuGluThrProGluLeuProLysProGlyValThrProArgSerGlu 181
                                       GCGTCAACAAGTGCATCGGCTTCAGCATCAACGAGTGCGTCCGCTTCAGCAAGTACTAGC
                                                                                                                             SerIleGluGluAlaSerLysSerMetGluSerThrLeuGluSerLeuGlnSerLeuSer 141
                                                                    AlaAlaGlnMetLysGluValGluAlaValValAlaAlaLeuSerGlyLysSerSer 161
                                                                                                  ----GAATCGGCATCAACGAGTGCGTCCGCTTCAGCAAGTACTAGCGCCTCAGCCTCA
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HP Vectra 486/33
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Conservative:
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RESULT 14 US-08-961-527-367

Sequence 367, Application US/08961527
Patent No. 6420135
GENERAL INFORMATION:
APPLICANT: Charles Kunsch

TITLE OF INVENTION:

Streptococcus pneumoniae Polynucleotides and Sequences

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ValMetIleAlaValSerValAlaIleThrValIleSerIleValAlaAlaIlePheThr 278
                                                                                                                                                                                                                                                                                                                                         AGTACCAGTGCGTCGGCTTCAGCATCAACGAGTGCTTCAGTCTCAGCGTCAACCAGTGCC
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                                                                                                                                                                                                                                                                     GlyValGlyValValValAlaAlaProAlaLeuGlyLysGlyIleMetGlnMetGlnLeu 417
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CTCGGCTTCAGCAAGTACCAGTGCGTCAGCTTCAGCAAG-CACAAGTGCGTCAGCTTC
                           uLysalaTyralaAlaIleSerGlyAlaIleAlaGlyAlaHisLysThrAsnAsnPhe 496
                                                                                                                                                                                                      CTGAATCTGCATCAACCAGTGCGTCACTTCCGC-----ATCAACAAGCGCCTCGGCCTC 1944
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                                                                 ATCAACCAGTGCATCAGCTTCAGCCTCAACAAGTGCTTCAGCCTCAGCGTCAACCAGTGC 2031
                                                                                              sGlnThrGlyGluSerAsnGluMetThrGlnLysAlaThrLysLeuGlyAlaGlnIleLe 477
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                                                                                                                                                                                                                                                      32546 GCCTCCGCAGCAGCAGCCTCAAAAACAGCGGCTGCATTATCTGCCAGTGCCGCGTCAACA 32605
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INFORMATION FOR SEQ ID NO: 72:
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                                                                                                                                                                                                 160 SerSerGlySerAlaLysLeuGluThrProGluLeuProLysProGlyValThrProArg 179
                                                                                                                                                                                                                                                                                                                                                                        120 GlnThrSerIleGluGluAlaSerLysSerMetGluSerThrLeuGluSerLeuGlnSer 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                  102 ValSerGlyAlaAla-----AlaThrThrAlaSerAsnThrAlaThrLysIleAlaMet 119
                                       200 ThrLysSerAlaLeuSerAsnTyrAlaSerThrGlnAlaGlnAlaAspGlnThrAsnLys 219
                                                                                                                                                                                                                                                                                           140 LeuSerAlaAlaGlnMetLysGluValGluAlaValValAlaAlaLeuSerGlyLys 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 SerIleSerSerSerGlyProAspAsnGlnLysAsnIleMetSerGlnValLeuThr 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SerGlyLysAspLysThrSer---SerThrThrLysThrGluThrAlaProGln------
                                                                                     AGTGCCGCATCGTCTGCTTCAACAGCCACAACGAAGGCT
                                                                                                                             SerGluValIleGluIleGlyLeuAlaLeuAlaLysAlaIleGlnThrLeuGlyGluAla 199
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STRANDEDNESS: double
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	ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland	AD CI ST	
Sequences	327-363 363, Application US/08961527 3. 6420135 INFORMATION: CHARLES Kunsch OF INVENTION: Streptococcus pneumoniae Polynucleotides and R OF SEQUENCES: 391 SPONDENCE ADDRESS:	S-08-961-5: Sequence Sequence Patent No GENERAL APPLIC TITLE NUMBER CORRES	
	GCAGCTAATGATAAT	33407	Db
	AlaIleSerGlyAlaIleAlaGlyAlaHisLysThrAsn 494	4	Qy
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481	hrLysLeuGlyAlaGlnIleLeuLysAlaTyrAla	462	Qy
461 33346	SerMetPheThrGlnPheTrpGlnGlnAlaSerLysIleAlaSerLysGlnThrGlyGlu :::	442 33293	Qy Db
33292	AAAGGCAGCCTATGACCTTGCT	33248	Db
441	GlnAsnValAlaGlnPheGlnLysGluValGlyLysLeuGlnAlaAlaAlaAlaAlaAleuslle	422	Qy
33247	ACAGCACAGAAAGGGATAGTTCAGCTTAGCAACGCGACCAACAGCACATCTGAAATG	33191	Db QY
33190	AAAGCCGTTAAGGCCGCGTATGAGCTGGCTAACGGGAAATACACCGCACAGGATGCAACG	33131	Db
•	GlyvalValAlaAlaProAlaLeuGly		Qy
33130	ATAGTACAGCTCAGCAGTGCGACTAACAGCACTTCCGAGTCACTGGCGGCAACGCCA	33074	Db
399	PheProLysLeuSerLysValIleSerSerLeuThrSerLysTrpValThrValGlyVal	380	Qy
379 33073	AlaileSerLysGlyIleSerLysValPheAlaLysGlyThrGlnMetIleAlaLysAsn	360 33014	Фр
33013	Ð	œ	Db
	AlaAlaValLysSerGlyIleLysAlaPheIleLysThrLeuValLysAlaIleAlaLys	ω	Qy
32983		32939	Db
339	GlnAlaValLysGlnAlaValIleThrAlaValArgGlnAlaIleThrAlaAlaIleLys	. 320	Qy
32938	TCAGCAGCGAAGAGCAGCGCCACGGCATCCACGAAGGCGACAGAGGCAGCT	32885	Db
319	AlaAlaGlyAlaAlaAlaAlaThrThrValAlaThrGlnIleThrValGlnAlaValVal	300	Qγ
32884	CTGCTTCAAAAGATGAGGCGACCAGACAAGCG	32825	Db
299	AlaGlyGly	280	Qу
32824	TCGTCAGCCAGT	32804	Db
279	MetIleAlaValSerValAlaIleThrValIleSerIleValAlaAlaIlePheThrCys	260	Qy
32803	AAGACATCCGAAACGAACGCGAAAGCGTTGGAAAACCAGCGCAGAATCCTCAAAAAACG	32747	Db
259	aAlaGluGlnLysSerLysAspLeuGluGlyThrMetAspThrValAsnThrVal	240	Qy
32746		32744	Db
239	LeuGly LeuGluLysGlnAlaIleLysIleAspLysGluArgGluGluTyrGlnGluMet	220	Qy

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5417 TCAACGAGTGCCTCAGCCTCAGCAAGTATCTCAGCGTCTGAATCGGCATCAACGAGTGCG 5476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82 GlnGlyValAlaAlaGlyLysGluSerSerGluSerGlnLysAlaGlyAlaAspThrGly 101
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                                                                                                                                                                                                                                                                                 198 GlualaThrLysSerAlaLeuSerAsnTyrAlaSerThrGlnAlaGlnAlaAspGlnThr 217
                            278 ThrCysGlyAlaGlyLeuAlaGlyLeuAlaAlaGlyAlaAlaValGlyAlaAlaAlaAla 297
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                                                                                                                                                                                                                                                                                                                                                ProArgSerGluValIleGluIleGlyLeuAlaLeuAlaLysAlaIleGlnThrLeuGly 197
                                                                                                                                                                                                                                                                                                                                                                                 GCCTCAACAAGTGCTTCAGCCTCAGCGTCAACCAGTGCCTCGGCTTCAGCAAGTACCAGT 5137
                                                                                                                                                                                                                                                                                                                                                                                                      GlyLysSerSerGlySerAlaLysLeuGluThrProGluLeuProLysProGlyValThr 177
                                                                                           ThrvalMetIleAlaValSerValAlaIleThrValIleSerIleValAlaAlaIlePhe 277
                                                                                                                           AGTATCTCAGCGTCTGAATCGGCATCAACGAGTGCATCAGCATCAGCATCAACGAGTGCA 5356
                                                                                                                                                         GluMetLysAlaAlaGluGlnLysSerLysAspLeuGluGlyThrMetAspThrValAsn 257
                                                                                                                                                                                        ACT-----AGTGCATCAGCATCAGCATCAACÇAGTGCATCAGCCTCAGCA 5296
                                                                                                                                                                                                                      AsnLysLeuGlyLeuGluLysGlnAlaIleLysIleAspLysGluArgGluGluTyrGln 237
                                                                                                                                                                                                                                                        GCATCAACAAGTGCCTCAGCATCA-----GCATCAACGAGTGCGTCAGCCTCAGCAAGT 5251
                                                              TOGGCTTCAGCGTCAACCAGTGCATCAGTCTCAGCAAGCACCAGTGCGTCGGCTTCAGCA 5416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6e-10
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Indels:
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NESULT 12 US-09-453-702B-72 US-09-453-702B-72  Sequence 72, Application US/09453702B  Patch No. 6365723el Sequences of E. coli O157  NUMBER OF SEQUENCES: 265  CORRESPONDENCE ADDRESS: ADDRESSE: Quarles & Brady STREET: 1 South Pinckney Street CITY: Madison STATE: WI COUNTRY: US ZIE: 53701-2113 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage COMPUTER TIBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Word Perfect 8.0  CURRENT APPLICATION NUMBER: US/09/453,702B FILLING DATE: 03-Dec-1999  CLASSIFICATION DATA: PRIOR APPLICATION DATA:	472	5962 GTTGGAAAT	459 ThrGlyGluSerAsnGluMetThrGlnLySAlaThrLyS	450 GlnalaSerLySileAlaSer	437 Ala	5798CCTCAACAAGTGCG	418	л	378 LysasnPheProLysLeuSerLysValIILeSerSerLeuThrScrLysIIPvalIII.va.	5654 GCA	358 AlaLysAlaIleSerLysGlyIleSerLysValPheAlaLysGlyThrGlnMetIleAla 3	338 IleLysAlaAlaValLysSerGlyIleLysAlaPheIleLysThrLeuvalLysAlaLie	5537 T	318 ValValGlnAlaValLysGlnAlaValIleThrAlaValArgGlnAlaIleThrAlaAla	298 GlyGlyAlaAlaGlyAlaAlaAlaAlaThrThrValAlaThrGlnIleThrValGlnAla 317

355	AlaAlaIleLysAlaAlaValLysSerGlyIleLysAlaPheIleLysThrLeuValLys	336	. Q
1687	GAAGGCGGCGACGGGAGTGTCGTTTATTCAGCAGGCG	1643	DЬ
335	leThrAlaValArgGlnAlaIl ::::: :::::!     :::	317	Qy
1642		1625	DЬ
316	AlaGlyGlyAlaAlaGlyAlaAlaAlaAlaThrThrValAlaThrGlnIleThrValGln	297	Qy
296 1624	PheThrCysGlyAlaGlyLeuAlaGlyLeuAlaAlaGlyAlaAlaValGlyAlaAlaAla	277 1577	ОУ
276 1576	ASnThrValMetIleAlaValSerValAlaIleThrValIleSerIleValAlaAlaIle	257 1526	D 99
256 1525	GlnGluMetLysAlaAlaGluGlnLysSerLysAspLeuGluGlyThrMetAspThrVal	237 1475	рь
236 1474	ThrasnLysLeuGlyLeuGluLysGlnalaIleLysIleAspLysGluArgGluGluTyr	217 1418	D Qy
216 1417	GlyGluAlaThrLysSerAlaLeuSerAsnTyrAlaSerThrGlnAlaGlnAlaAspGln    ::    :: ::          GGCAAAAATACGGAAGAAAGCCTGCAAAACGATCTTGCGCTT	197 1376	Оy
196 1375	ProArgSerGluValIleGluIleGlyLeuAlaLeuAlaLysAlaIleGlnThrLeu	178 1316	Qу
177 1315	GlyLysSerSerGlySerAlaLysLeuGluThrProGluLeuProLysProGlyValThr	158 1256	ОУ
157 1255	AlaGlnMetLysGluValGluAlaValValAlaAlaLeuSer	143 1196	Qу
142 1195	IleGluGluAlaSerLysSerMetGluSerThrLeuGluSerLeuGlnSerLeuSerAla :::   :::	123 1136	Оy
122 1135	SerGlyAlaAlaAlaThrThrAlaSerAsnThrAlaThrLysIleAlaMetGlnThrSer:::	103 1118	Db Qy
102 1117	LysGluSerSerGluSerGlnLysAlaGlyAlaAspThrGlyVal	1058	pb 04
87 1057	AspLysThrSerSerThrThrLysThrGluThrAlaProGlnGlnGlyValAlaAlaGly	1019	Qу
67 1018	ArgGlnGlyLysAsnThrGluMetGluSerAspAlaThrIlealaGlyAlaSerGlyLys	48 968	Qy Db
47 967	GlnGlyValProGlnGlnAspLysLeuSerGlyAsnGlu   GlnGlyValProGlnGlnAspLysLeuSerGlyAsnGlu   I	908	Db Qy
	milarity: 41.02% Con Similarity: 23.67% Mis h: 9.22% Ind 2 Gap	cent s t Loca ry Mat	Per Bes Que

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FILP FILP FILP FILP FILP NAM REG REG REF REG REF REG REF REG REF REG REF REG REF REG REF REG REG REG REG REG REG REG REG REG REG	Patent No. 6420135  Patent No. 6420135  GENERAL INFORMATION: APPLICANT: Charles Kunsch APPLICANT: Charles Kunsch TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences NUMBER OF SEQUENCES: 391  CORRESPONDENCE ADDRESS: ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: USA ZIP: 20850  COMPUTER: MARYLAND COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: READABLE FORM: MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: ASCII Text CURRENT APPLICATION NUMBER: US/08/961,527 FILING DATE: CLASSIFICATION NUMBER: US/08/961,527  PETING DATE: CLASSIFICATION 1424  BERTOR ADDRICATION 1424	450 GlnAlaSerLysIleAlaSerLysGlnThrGlyGlu 461 ::: 1944 CGTATTACTAGCGGTCTGGGTAATGTGGGTAAGAATGGCCTGAAACGAATGCCTTA 2053 462 SerAsnGluMetThrGlnLysAlaThrLysLeuGlyAlaGlnIleLeuLys 478	356 AlaIleAlaLysAlaIleSerLysGlyIleSerLysValPheAlaLysGlyThrGlnMet 3	1688 CCGATTATGGAGCATGTGCTGAAGCCGTTAATGGAG 1723

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987

88 LysGluSerSerGluSerGlnLysAla-----------GlyAlaAspThrGlyVal 102

AAAAACTGACGCAGGCGCAAAATAAATTGCAATCGCTGGACCCAGCTGACCCCGGCTAT 1085

SerGlyAlaAlaAlaThrThrAlaSerAsnThrAlaThrLysIleAlaMetGlnThrSer 122

AspLysThrSerSerThrThrLysThrGluThrAlaProGlnGlnGlyValAlaAlaGly 87

1026

103

Qy В QΥ В QУ

143 AlaGlnMetLys------GluValGluAlaValValAlaAlaLeuSer 157

GCGACGGTTAAAGCAGGCACAGACGCCAAAGCCGAAAGCCGAGAAAGCGGATAACATTCTG 1223

123 IleGluGluAlaSerLysSerMetGluSerThrLeuGluSerLeuGlnSerLeuSerAla 142

1086 GCACAAGCTGAAGCC------GCG 1103

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1224 ACCAAATTCCAGGGAACGGCTAATGCCGCCTCTCAGAATCAGGTTTCCCCAGGGTGAGCAG 1283

158 GlyLysSerSerGlySerAlaLysLeuGluThrProGluLeuProLysProGlyValThr 177

1284 GATAATCTGTCAAATGTCGCCCGCCTCACTATGCTCATGGCCATGTTTATTGAGATTGTG 1343

178 ProArg---SerGluVallleGluIleGlyLeuAlaLeuAlaLysAlaIleGlnThrLeu 196

Вþ

망 Qy В QΥ

1386 TTCAACGCCTTGCAGGAAGGGCGTCAGGCG---GAGATGGAAAAAGAAATCGGCTGAATTC 1442

ThraspLysLeuGlyLeuGluLysGlnalaIleLysIleAspLysGluArgGluGluTyr 236 GGCAAAAATACGGAAGAAGCCTGCAAAACGATCTTGCGCTT------ 1385 GlyGluAlaThrLysSerAlaLeuSerAsnTyrAlaSerThrGlnAlaGlnAlaAspGln 216

1443 CAGGAA------GAGACGCGCAAAGCCGAGGAAACGAACCGCATTATGGGATGTATC 1493

GinGluMetLysAlaAlaGluGlnLysSerLysAspLeuGluGlyThrMetAspThrVal 256

AsnThrValMetIleAlaValSerValAlaIleThrValIleSerTleValAlaAlaIle 276

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AlaGlyGlyAlaAlaGlyAlaAlaAlaAlaThrThrValAlaThrGlnIleThrValGln 316

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1656 CCGATTATGGAGCATGTG-----

336 AlaAlaIleLysAlaAlaValLysSerGlyIleLysAlaPheIleLysThrLeuValLys 355

----CTGAAGCCGTTAATGGAG

1691

AlavalValGlnAlaValLysGlnAlaVal---IleThrAlaValArgGlnAlaIleThr 335

----GTGAAGGCGGCGACGGGGGTGTCGTTTATTCAGCAGGCGCTAAAC 1655

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1797 ATGGTAGCGGTCATTGTGGTGGTCGCAGTTGTCGGGAAAGGCGCGGCGGCGAAACTGGGT 1856

GATAAGAAAACGGCAGAGATGGCAGGCAGCATTGTTGGTGCGATTGTCGCCGCTATTGCC 1796 IleAlaLysAsnPheProLysLeuSerLysVallleSerSerLeuThrSerLysTrpVal 395 AlaileAlaLysAlaileSerLysGlyIleSerLysValPheAlaLysGlyThrGlnMet B

936 GCTCTGGGA-----GAGGCTCAGGAGGCGACGGATCTCTATGAAGCCAGCATCAAA 986

Alignment Scores: 5.26e-12 Length: 3622  Pred. No.: 5.26e-12 Matches: 116  Score: 218.50 Matches: 116	CORRESPONDENCE STORM FORESTER ADDRESSEE: DOOD Pennsylvania Avenue, NW STREET: 2000 Pennsylvania Avenue, NW CITY: Washington  CIVATE: DC COUNTRY: USA II 20006-1812 COMPUTER: ELDOPY disk MEDIUM TYPE: Floppy disk MEDIUM TO ANTA: SOPTWARE: LEVATION POLOTION MEDIUM FLOPPY MEDIUM TO ANTA: MEDIUM T	RESULT 10 US-08-591-079-7 US-08-591-079-7 ; Sequence 7, Application US/08591079 ; Patent No. 5972899 ; Patent No. 5972899 ; GENERAL INFORMATION: ; APPLICANT: Zychlinksky, Arturo ; APPLICANT: Chen, Yajing ; APPLICANT: Application induced by Shigella IpaB TITLE OF INVENTION: Apoptosis Induced by Shigella IpaB ; NUMBER OF SEQUENCES: 10 ; NUMBER OF SEQUENCES:	462 2022 479 2082	

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 В
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INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1296 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
 1084
                                                   1024
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: JP 10 FILING DATE: 28-APR-1995 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Miller, Charles REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 MetSerIleSerSerSerSerGlyProAspAsnGlnLysAsnIleMetSerGlnValLeu
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                                                                                                                                                                                                                                                                                                                                                                 GluGluAlaSerLysSerMetGluSerThrLeuGluSerLeuGlnSerLeuSerAlaAla 143
                                                                                                                                                                                                                                                                                                                                                                                                                      ATGTCTATTTCATCTTCAGGACCTGACAATCAAAAAAATATCATGTCTCAAGTTCTG
            LeuSerAsnTyrAlaSerThrGlnAlaGlnAlaAspGlnThrAsnLysLeuGlyLeuGlu
                                                                                                                  AlaLysLeuGluThrProGluLeuProLysProGlyValThrProArgSerGluValIle
                                                                                                                                                                     GlnMetLysGluValGluAlaValValValAlaAlaLeuSerGlyLysSerSerGlySer 163
                                                                                                                                                                                                                                                                          GlyAlaAlaAlaThrThrAlaSerAsnThrAlaThrLysIleAlaMetGlnThrSerIle
                                                                                                                                                                                                                                                                                                                GTTGCTGCTGGGAAAGAATCCTCAGAAAGTCAAAAGGCAGGTGCTGATACTGGAGTATCA
                                                                                                                                                                                                                                                                                                                              ValAlaAlaGlyLysGluSerSerGluSerGlnLysAlaGlyAlaAspThrGlyValSer 103
CAAATGAAAGAAGTCGAAGCGGTTGTTGTTGCTGCCCTCTCAGGGAAAAGTTCGGGTTCC
                                                                                                                                                                                                            GAAGAGGCGAGCAAAAGTATGGAGTCTACCTTAGAGTCACTTCAAAGCCTCAGTGCCGCG
                                                                                                                                                                                                                                                             GGAGCGGCTGCTACTACAGCATCAAATACTGCAACAAAAATTGCTATGCAGACCTCTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                IleGlnGlnThrArgGlnGlyLysAsnThrGluMetGluSerAspAlaThrIleAlaGly 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACATCGACACCCCAGGGCGTGCCCCAACAAGATAAGCTGTCTGGCAACGAAACGAAGCAA
                                                                                                      GCAAAATTGGAAACACCTGAGCTCCCCAAGCCCGGGGTGACAACCAAGATCAGAGGTTATC
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Matches:
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LOCATION: 543..232
OTHER INFORMATION:
US-08-591-079-9
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Best Local Similari
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TELEX: 90-4030 MRSNFOERSWSH
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Livnat, Shmuel
REGISTRATION NUMBER: 33,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 5393 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Zychlinksky, Arturo
APPLICANT: Chen, Yajing
                                                                                                                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               244 GlnLysSerLysAspLeuGluGlyThrMetAspThrValAsnThrValMetIleAla 262
                                                 876 CAGGCGATGATTGAGTCACAAAAAGAGATGGGGATTCAGGTATCGAAAGAATTCCAGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                 48
                                                                                                                                                                                                                                                                                                                                                                            STRAIN: Ty2
                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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ArgGlnGlyLysAsnThrGluMetGluSerAspAlaThrIleAlaGlyAlaSerGlyLys
                                                                                  GlnGlyValProGlnGlnAspLysLeuSerGlyAsnGluThrLysGlnIleGlnGlnThr 47
                                                                                                                                                                                      Similarity:
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23.67%
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Matches:
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NAME: Miller, Charles E.
REGISTRATION NUMBER: 24,576
REGISTRATION NUMBER: 7426-043-999
REFERENCE/DOCKET NUMBER: 7426-043-999
TELECOMBUNICATION INFORMATION:
TELEPHONE: (212) 790-9990
TELEPHONE: (212) 790-9990
TELEPHONE: (212) 790-9990
TELEPHONE: (212) 869-8864/9741
TELEX: 66141 PENNIE
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity:
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APPLICATION NUMBER: JP 106

FILING DATE: 28-APR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 106

APPLICATION NUMBER: JP 106

FILING DATE: 28-APR-1995
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APPLICATION NUMBER:
FILING DATE: 28-APR-
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 106006/95
FILING DATE: 28-APR-1995
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APPLICATION NUMBER: JP 106011/95
FILING DATE: 28-APR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid;
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                                                                        nucleic acid
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: ILM PC COMPATIBLE

COMPUTER: ILM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-OOS

OPERATING SYSTEM: 10-MAR-1997

FILING DATE: 19-MAR-1997

FILING DATE: 19-MAR-1997
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APPLICATION NUMBER: JP 224
APPLICATION NUMBER: JP 224
FILING DATE: 20-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 100
APPLICATION NUMBER: JP 100
APPLICATION DATA:
PRIOR APPLICATION DATA:
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STREET: 1155 Aver
CITY: New York
STATE: New York
                                                 APPLICATION NUMBER: FILING DATE: 28-APR-PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 1: FILING DATE: 28-APR-1995 PRIOR APPLICATION DATA:
                                                                                                       FILING DATE: 28-APR-
PRIOR APPLICATION DATA:
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Matsumoto, Akira
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pennie &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ON: CHLAMYDIA PNEUMONIAE ANTIGENIC POLYPEPTIDES,
ON: FUSED PROTEINS CONTAINING THE POLYPEPTIDES, DNAS CODING
ON: THEREFOR, RECOMBINANT VECTORS CARRYING THE DNAS, TRANSFORMA
ON: CONTAINING THE RECOMBINANT VECTORS, METHOD FOR PRODUCTION O
ON: ANTIBODY, METHOD AND REAGENTS FOR DETECTION AND/OR MEASUREM
ON: OF ANTIBODY, METHOD AND AGENTS FOR DIACNOSIS OF CHLAMYDIA
ON: PNEUMONIAE INFECTIONS, PROBES AND PRIMERS FOR DETECTION AND
ON: MEASUREMENT OF CHLAMYDIA PNEUMONIAE GENE, AND METHOD AND
ON: REAGENTS FOR DETECTION AND/OR MEASUREMENT OF CHLAMYDIA
ON: PNEUMONIAE GENE
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                                          JP 106010/95
                                                                                            JP 106009/95
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                                                                                                                                                                                                                                                                                                                                Score:
                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 28-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Miller, Charles E.
REGISTRATION NUMBER: 24,576
REFERENCE/DOCKET NUMBER: 7426-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 869-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 777 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: JP 106
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 106
FILING DATE: 28-APR-1995
PRIOR APPLICATION NUMBER: JP 106
                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
TOPOLOGY: lin
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 10
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                    Match:
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181
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FILING DATE: 28-APR-1995
RIDR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
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                                                                                                                                                                                          4 MetSerIleSerSerSerSerGlyProAspAsnGlnLysAsnIleMetSerGlnValLeu
                                                                                                                 AlaSerGlyLysAspLysThrSerSerThrThrLysThrGluThrAlaProGlnGlnGly
                                                       GCTTCTGGAAAAGACAAAACTTCCTCGACTACAAAAACAGAAAACAGCTCCACAACAGGGA
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
TITLE OF INVENTION:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                            SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
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                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                APPLICATION NUMBER: US/0 FILING DATE: 19-MAR-1997
                                                                                                                                                                                                                STATE: New York
                                                                                                                                                                                                                                     CITY:
                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                    ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GlyAlaAlaAlaThrThrAlaSerAsnThrAlaThrLysIleAlaMetGlnThrSerIle 123
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10036-2711
                                                                                                                                                                                                                                   New York
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Obara, Kazuhiko
Matsumoto, Akira
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                                                                                                                                                                                                                                                 Pennie & Avenue
                                                                                                                                                                                                                                                                                                                                                 CHLAMYDIA PNEUMONIAE ANTIGENIC POLYPEPTIDES,
FUSED PROTEINS CONTAINING THE POLYPEPTIDES,
THEREFOR, RECOMBINANT VECTORS CARRYING THE DNAS, TRANSFORMA
CONTAINING THE RECOMBINANT VECTORS, METHOD FOR PRODUCTION O
ANTIBODY, METHOD AND REAGENTS FOR DETECTION AND/OR MEASUREM
OF ANTIBODY, METHOD AND AGENTS FOR DIAGNOSIS OF CHLAMYDIA
PNEUMONIAE INFECTIONS, PROBES AND PRIMERS FOR DETECTION AND
MEASUREMENT OF CHLAMYDIA PNEUMONIAE GENE, AND METHOD AND
                                                                                                                                                                                                                                                                                                                   REAGENTS FOR DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US/08809326A
                                                                                                 Release #1.0, Version #1.30
                                                                  US/08/809,326A
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of the Ameri
 JP 224711/94
                                                                                                                                                                                                                                                     the Americas
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В

287 CAAGTTCTGACATCGACACCCCAGGGCGTGCCCCAACAAGATAAGCTGTCTGGCCAACGAA 346

COMPUTER: IMP PC COMPATIBLE
COMPUTER: IMP PC -DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,326A
FILING DATE: 19-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 224711/94
FILING DATE: 20-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 224711/94
FILING DATE: 20-SEP-1994
PRIOR APPLICATION DATA:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

CITY: New York
STATE: New York

COUNTRY:

USA

RESULT US-08-4 Pactes Pates Pa	Qy Db	Qy Db	Qу	Qу	Qy Db	Фу	Фу	Qy	Qy Db	Qy	Qy Db	ОУ
SULT 6 -08-809-326A-7	261 IleAla 262        1007 ATCGCG 1012	241 AlaAlaGluGlnLysSerLysAspLeuGluGlyThrMetAspThrValAsnThrValMet 200					, , P					0 4 0

PRIOR APPLICATION UNITE:

PRIOR APPLICATION NUMBER: JP 106006/95

FILING DATE: 28-APR-1995

PRIOR APPLICATION UNBER: JP 106008/95

PRIOR APPLICATION UNMBER: JP 106008/95

PRIOR APPLICATION UNMBER: JP 106009/95

FILING DATE: 28-APR-1995

PRIOR APPLICATION UNMBER: JP 106010/95

FILING DATE: 28-APR-1995

PRIOR APPLICATION UNMBER: JP 106011/95

FILING DATE: 28-APR-1995

PRIOR APPLICATION UNMBER: JP 106011/95

FILING DATE: 28-APR-1995

APPLICATION UNMBER: JP 106011/95

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APPLICATION UNMBER: JP 106011/95

FILING DATE: 28-APR-1995

FILING APPLICATION UNMBER: JP 106011/95

FILING DATE: 28-APR-1995

FILING APPLICATION UNMBER: JP 106011/95

FILING APPLICATION UNMB

7426-043-999

Percent Similarity:
Best Local Similarity:
Query Match:
DB:

1.95e-118 1262.00 100.00% 100.00% 53.27%

Length: Matches:

1048 262 0 0 0

Alignment Scores: US-08-809-326A-9

FEATURE:

NAME/KEY: CDS LOCATION: 236 to 1012 IDENTIFICATION METHOD:

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IMMEDIATE SOURCE: CLONE: 53-3S

STRAIN:

YK-41

ORGANISM: Chlamydia pneumoniae

MOLECULE TYPE: ORIGINAL SOURCE:

TYPE: nucleic acid

ENGTH:

1048 base pairs

STRANDEDNESS: TOPOLOGY:

linear

Genomic DNA double

. No.:

US-09-889-314-2 (1-496) x US-08-809-326A-9 (1-1048)

Gaps: Mismatches: Indels: Conservative:

20

21 GlnValLeuThrSerThrProGlnGlyValProGlnGlnAspLysLeuSerGlyAsnGlu

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Query Match:
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                                                                                                                                                                                                                                      AlaSerGlyLysAspLysThrSerSerThrThrLysThrGluThrAlaProGlnGlnGly 83
                                                                                                                                                                                                                                                                                                                                                                                                      AlaLySLeuGluThrProGluLeuProLySProGlyValThrProArgSerGluValIle 183
                                                                                                                                                                                                           GlyAlaAlaAlaThrThrAlaSerAsnThrAlaThrLysIleAlaMetGlnThrSerIle 123
                                                                                                                                                                                                                                                                                          ThrSerThrProGlnGlyValProGlnGlnAspLysLeuSerGlyAsnGluThrLysGln 43
                                                                           GlnLysSerLysAspLeuGluGlyThrMetAspThrValAsnThrValMetIleAlaVal 263
                                                                                                       LysGlnAlaIleLysIleAspLysGluArgGluGluTyrGlnGluMetLysAlaAlaGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scores:
   GlyAlaAla
                 ATGATCCTCTACGCCGGACGCATCGTTGGCCGGCATCACCGGCGCCACAGGTGCGGTTGCT
                        AlaIlePheThrCysGlyAlaGlyLeuAlaGlyLeu-----AlaAlaGlyAlaAlaVal
                                                                     CAGAAGTCTAAAAGATCTCGAAGGAACAATGGATACTGTCAATACTGTGATGATCGCGAA- 1318
                                                                                                AAGCAAGCGATAAAAATCGATAAAGAACGAGAAGAATACCAAGAGATGAAGGCTGCCGAA
                                                                                                                                                                                                                                                                 GGAGCGGCTGCTACTACAGCATCAAATACTGCAACAAAAATTGCTATGCAGACCTCTATT
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1265.00
62.39%
56.42%
53.40%
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  (1-5438)
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312
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135
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                 1438
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	; ADDRESSEE: Pennie & Edmonds LLP ; STREET: 1155 Avenue of the Americas	
	CORRESPONDENCE ADDRESS:	
	TITLE OF INVENTION:	
CHLAMYDIA	TITLE OF	
0	TITLE OF INVENTION: PNEUMONIAE INFECTIONS, PROBES AND PRIMERS FO	
AND/OR MEASUREM	TITLE OF INVENTION: ANTIBODY, METHOD AND REAGENTS FOR DETECTION	
FOR PRODUCTION O	TITLE OF INVENTION: CONTAINING THE RECOMBINANT VE	
DNAS, TRANSFORMA	TITLE OF INVENTION: FUSED PROTEINS CONTAINING THE PUBLIFEFTIDES,	
	TITLE OF INVENTION: CHLAMYDIA PNEUMONIAE ANTIGENIC POLYPEPTIDES.	
	; APPLICANI: Obdia, Nazuniko ; APPLICANI: Matsumoto, Akira	
	APPLICANT: Izutsu, I	
	GENERAL IN	
	ence	
	RESULT 5 US-08-809-326A-9	
	LO1GGATCGCTCGCGGCTCTTACCAGCCTAACTTC	
	Qy 431 VAIGIYLYSLEUGINALAALAALAASPMETILESETMET 443	
2100	2041 CCCGCGTTGCAGGCCATGCTGTCCAGGCAGGTAGATGACGAC	
	110	
430	Ov 411 GlvīleMetGlnMetGlnLeuSerGluMetGlnGlnAsnValAlaGlnDheGlnLvsGlu	
2040	Db 1981 ACGCGAGGCTGGATGGCCTTCCCCATTATGATTCTTCTCGCTTCCGGCGGCATCGGGATG	
410	Qy 391 ThrSerLysTrpValThrValGlyValGlyValValValAlaAlaProAlaLeuGlyLys	
1980	Db 1921 CAGGCCATTATCGCCGGCATGGCGGCCGACGCGCTGGGCTACGTCTTGCTGGCGTTCGCG	
390	Qy 384 SerLysVallleSerSerLeu	
1920	Db 1891 GGTCCCGCC	
383	Qy 364 GlyIleSerLysValPheAlaLysGlyThrGlnMetIleAlaLysAsnPheProLysLeu	
1890	Db 1831 ATCGGCCTGTCGCTTGCGGTATTCGGAATCTTGCACGCCCTCGCTCAAGCCTTCGTCACT	
363	Qy 344 SerGlyIleLysAlaPheIleLysThrLeuValLysAlaIleAlaLysAlaIleSerLys	
1830	Db 1771 GTGCCGGCAGCGCTCTGGGTCATTTTCGGCGAGGACCGCTTTCGCTGGAGCGCGACGATG	
343	Qy 334 IleThrAlaAlaIleLysAlaAlaValLys	
1770	Db 1738 ACTGTCTTTATCATGCAACTCGTAGGACAG	
333	Qy 314 ThrvalGlnAlaValValGlnAlaValLysGlnAlaValIleThrAlaValArgGlnAla	
1737	Db 1678 TTCAACCCAGTCAGCTCCTTCCGGTGGGCGCGGGGCATGACTATCGTCGCCGCACTTATG	
313	laThrGlnI	
1677	Db 1618 GGCTGCTTCCTAATGCAGGAGTCGCATAAGGGAGAGCGTCGACCGATGCCCTTGAGAGCC	
306	Qy 306	
1617	Db 1558 ATCTCCTTGCATGCACCATTCCTTGCGGCGGCGGTGCTCAACGGCCTCAACCTACTACTG	
306	Qy 304AlaAlaAla	
1557	Db 1498 GAGCGCTTGTTTCGGCGTGGGTATGGTGGCAGGCCCGTGGCCGGGGGACTGTTGGGCGCC	
303	Qy 296AlahlaGiyalahlaGiyala	
1497	Db 1439 GGCGCCTA-TATCGCCGACATCACCGATGGGGAAGATCGGGCTCGCCACTTCGGGCTCAT	

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TYPE	Db 2252 ATCGGGATGCCGGGTTGCAGGCCATGCTGTCCAGGCAGGTAGATGACGACCATCAGGGA 2311	무 5
TYPE: nucleic acid : STRANDEDNESS: double	2192 GCGTTCGCGACGCGAGGCTGGATGGCCTTCCCCCATTATGATTCTTCTCCGCCTACTATGATTCTTCTCCGCCCCCATTATGATTCTTCTTCTCCGCCCCCATTATGATTCTTCTTCTCCGCCCCCCATTATGATTCTTCTTCTCCGCCCCCCCC	` ∺
CHARACTERISTICS: 5438 base pairs	2y 391ThrSerLysTrpValThrValGlyValGlyValValValAlaAlaPrOAla 407	$\sim$
; TELEPHONE: (212) /90-9090;; TELEX: 66141 PENNIE; TELEX: 66141 PENNIE; 25:	381 ProLysLeuSerLysValIleSerSerLeu	₽ ₹
NAME: MILLEY, CHARLES E. REGISTRATION NUMBER: 24,576 REFERENCE/DOCKET NUMBER: 7426-043-999 TELECOMMUNICATION INFORMATION:	361 IleSerLysGlyIleSerLysValPneAlaLysGlyIllGlimGCLICACAAACGTTTC 2102 TTCGTCACTGGTCCCGCC	₽ ₹
Z H	341 AlaValLysSerGlyIleLysAlaPhelleLysThrLouValLysAlaLleAlacysAla	ر بر
FILING DATE: 28-APR-1995 PRIOR APPLICATION NUMBER: JP 106010/95 APPLICATION NUMBER: JP 106010/95 FILING DATE: 28-APR-1995	331 ArgGlnAlaIleThrAlaAlaIle	₹ ₹
APPLICATION NUMBER: JF 106008/95 FILING DATE: 28-APR-1995 PRIOR APPLICATION DATA: APPLICATION NUMBER: JF 106009/95	311 1949	9 4
P 70 1	307	₽ Ч
PRIOR APPLICATION DATA: APPLICATION NUMBER: JP 224711/94 FILING DATE: 20-SEP-1994	_	σ -
CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/809,326A FILING DATE: 19-MAR-1997 CLASSIFICATION: 435	11111 1769 TTGGGCGCCATCTCCTTGCATGCACCATTCCTTGCGGCGGGGGGGG	, 0
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30	CGGGCTCATGAGCGCTTGTTTCGGCGTGGGTAT	, ,
STATE: New FOLK COUNTRY: USA ZIP: 10036-2711 COMPUTER READABLE FORM:	1650 GCGGTTGCTGGCCCTA-TATCGCCGACATCACCGATGGGGAAGATCGGGCTCGCCACTT 1708  296AlaalaG1yG1yAla 300	
ADDRESSEE: Pennie & Edmonds LLP STREET: 1155 Avenue of the Americas CITY: New York	TAATCGATGA AlavalGlyA	
TITLE OF INVENTION PREDMONIAE GENE TITLE OF INVENTION: PREDMONIAE GENE NUMBER OF SEQUENCES: 31 CORRESPONDENCE ADDRESS:		
OF INVENTION: OF INVENTION:	261 IleAlaValSerValAlaIleThrVal	
OF INVENTION: OF INVENTION: OF INVENTION:	241 AlaAlaGluGlnLysSerLysAspLeuGluGlyThrMetAspThrValAsnThrValMet 260	
Obara, Ka Matsumoto NVENTION:		
RR 65P		
л ().	181 GluValIleGlyLeuAlaLeuAlaLysAlaIleGlnThrLeuGlyGluAlaThr 200 	
Qy 428 G1nLysG1uVa1G1yLysLeuG1nAlaAlaAlaAspMetIleSerMe		

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IN. CHLAMYDIA PNEUMONIAE ANTIGENIC POLYPEPTIDES,

NI. CHLAMYDIA PNEUMONIAE ANTIGENIC POLYPEPTIDES, DNAS CODING

IN. FUSED PROTEINS CONTALNING THE POLYPEPTIDES, DNAS CODING

IN. CHLAMYDIA PRECOMBINANT VECTORS CARRYING THE DNAS, TRANSFORMA

IN. THEREFOR, RECOMBINANT VECTORS, METHOD FOR PRODUCTION O

IN. CONTALNING THE RECOMBINANT VECTORS, METHOD FOR PRODUCTION O

IN. ANTIBODY, METHOD AND REAGENTS FOR DETECTION AND/OR MEASUREM

IN. OF ANTIBODY, METHOD AND AGENTS FOR DIFECTION AND

IN. MEASUREMENT OF CHLAMYDIA PNEUMONIAE GENE, AND METHOD AND

IN. REAGENTS FOR DETECTION AND/OR MEASUREMENT OF CHLAMYDIA

IN. REAGENTS FOR DETECTION AND/OR MEASUREMENT OF CHLAMYDIA

IN. PABUMONIAE GENE
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                                                   ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATINE SYSTEM: PC-DOS/MS-DOS
SOFTWARR: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION: 435
PRIOR APPLICATION UMBER: US/08/809,326A
FILING DATE: 19-MAR-1997
CLASSIFICATION UMBER: JP 224711/94
ETILING DATE: 70-SEP-1994
ETILING DATE: 70-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1 Patent No.
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   FILING DATE: 20-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 10
FILING DATE: 28-APR-1995
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F INVENTION:
F INVENTION:
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                                                                                                                                                                                                                                                                                                                                                             CHLAMYDIA PNEUMONIAE ANTIGENIC POLYPEPTIDES,
FUSED PROTEINS CONTAINING THE POLYPEPTIDES,
THEREFOR, RECOMBINANT VECTORS CARRYING THE DNAS, TRANSFORMANTS
CONTAINING THE RECOMBINANT VECTORS, METHOD FOR PRODUCTION OF
ANTIBODY, METHOD AND REAGENTS FOR DETECTION AND/OR MEASUREMENT
OF ANTIBODY, METHOD AND AGENTS FOR DIAGNOSTS OF CHLAMYDIA
PNEUMONIAE INFECTIONS, PROBES AND PRIMERS FOR DETECTION AND/OR
MEASUREMENT OF CHLAMYDIA PNEUMONIAE GENE, AND METHOD AND
REAGENTS FOR DETECTION AND/OR MEASUREMENT OF CHLAMYDIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hiroshi
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                  JP 106006/95
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-889-314-2 (1-496) x US-08-809-326A-10 (1-5658)
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
                                               1171
                                                                                                                                                                 1051
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 28-APR-PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
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SerGlySerAlaLysLeuGluThrProGluLeuProLysProGlyValThrProArgSer
                                                                                                     GlyValSerGlyAlaAlaAlaThrThrAlaSerAsnThrAlaThrLySIleAlaMetGln
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                                                              SerAlaAlaGlnMetLysGluValGluAlaValValAlaAlaLaLeuSerGlyLysSer 160
                                               AGTGCCGCGCAAATGAAAGAAGTCGAAGCGGTTGTTGTTGCTGCCCTCTCAGGGAAAAGT
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(212) 869-8864/9741
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56.65%
54.12%
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sequence 17, Application US/08809326A Patent No. 6165478
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                                                                 Alignment Scores: Pred. No.:
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Percent Similarity:
Best Local Similarity:
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FILING DATE: 19-MAR-1997
CLASSIETCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 224711/94
FILING DATE: 20-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 106006/95
FILING DATE: 28-APR-1995
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
10 106006/95
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FILING DATE: 28-APR-1995
PRIOR APPLICATION NUMBER: JP 106009/95
FILING DATE: 28-APR-1995
FILING DATE: 28-APR-1995
PRIOR APPLICATION NUMBER: JP 106010/95
FILING DATE: 28-APR-1995
FILING DATE: 28-APR-1995
PRIOR APPLICATION NUMBER: JP 106011/95
FILING DATE: 28-APR-1995
APPLICATION NUMBER: JP 106011/95
FILING DATE: 28-APR-1995
APTORNEY/AGENT INFORMATION:
NAME: Miller, Charles E:
NAME: Miller, Charles E:
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TELEX: (212) 790-9090
TELEPAN: (212) 869-8864/9741
TELEX: 66141 PENNIE
                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PATEN: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
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LENGTH: 1947 base pairs
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Obara, Kazuhiko
Matsumoto, Akira
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19-MAR-1997
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                                                                                                                                                             Other nucleic acid; Synthetic DNA
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                                                        Length: Matches:
              Conservative: Mismatches:
                                                               1947
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Db	Qy	Оу	Qy Db	Оу	Qy Db	Qу	Qy .	ДУ	ОУ	Qy Db	Qy	Оу	Qy Db	Qy .	Qy Db	Qу	Qу	US-09-	Query DB:
144	3 2	30 138	28 132	26 126	24 120	224 1144	204 1084	184 1024	164 964	144 904	124 844	104 784	84 724	64 664	44 604	24 544	484	889-	Match
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AGCTG	Alav	.aAlaA       TGCCG	GlyL        GGAC	erValAl         TGTTGC	LysSe        AAGTC	GlnAl         CAAGC	erAs      CTAA	IleG1	SLE HII	letLys       \TGAAA	luAla        aGGCG	laAla        CGGCT	laAla        CTGCT	erGly:	nGlnT       AGCAAA	rThrP        GACAC	riles       TATTT	(1-4	
>> −	- 11	laThrT         CAACCA	euAla        TCGCT	alle       CATT	rLysa         TAAAG	aile      GAT <i>i</i>	nTYTA       CTATG	yLeuA       ;acrcg	uGluT	SG1uVa        \GAAGT	SerI      AGC/	AlaTh        GCTAC	GlyLy        GGGAA	LysAs        AAAGA	hr Ar            CACG	rog1	erSe	96) x	9 4
CAGC	ThrAl	hr Va	AlaG1 11111 GCGGG	ThrVa.	SPLeu        ATCTC	LYSI1e	laSer        CAAGT	laLeu        CGCTT	hrPro        CACCT	1Glu       CGAA	ysserm        \AAAGTA	TACAC	SGLuS        AGAAT	PLYST        CAAAA	gGlnG        TCAGG	nGlyVa        \GGGCGT	rserse	US-0	7.76%
TGTC	aValA	lAlaTi         AGCAA	yAlaAli         AGCTGC	111es	GluG      GAAG	ASPLY        GATAA	ThrG1	AlaLy        GCTAA	GluLe       GAGCT	Alava        GCGGT	MetGlu        \TGGAG	lase	erSer        CCTCA	hrSer	llyLysA         GTAAAA	IPro GCCC	erGlyP        AGGAC	9-809	
GACA	rgGln	hrGln        CACAA	aVal      TGTA	TATI	lyThri        GAACA	SG1u       AGAP	nAla      AGCA	ysAlaI         AAGCAA	CCCC	IVal       GTT	SerThr	erAsnTh         AAATAC	GluSe         GAAAG	rSerTh	AsnThro	GlnGl        CAACA	ProAsp         CTGAC	)-326A	6 н
GCGA	Alail	leTh        ATTAC	GlyAl        GGTGC	ValAL        GTTGC	MetAs        ATGGA	ArgG1u         CGAGAA	lnA     AAG	leGln        TTCAG	yspro       AGCCC	3CT	hrLeuG         CCTTAG	rAlaT         TGCAA	rGlr 	hrThrL        CTACAA	rGluMe        TGAGAT	nAspLy         AGATAA	AsnG      AATC	-17	ndels aps:
CACC	eThr	TValG	aAlaA        AGCGG	aAla      TGCT	PThrV        TACTG	GAAT	AspG        GACC	ThrLe	_ ∩ − c	laLe	luSe      AGTC	TrLy CAAP	ysal          AGGC	ysThr        AAACA	etGlus         TGGAAA	CCI FI	InLys        AAAAA	1-19	::
ceec	AlaAla 	lnAla        AAGCT	LaA     CAG	EPh TTT	AT S	ACCAA	Thr ACA	euG LyG         GGGAG	GAC!	uSer	rLeuG        ACTTC	ILe?	GlyA       GGTG	GLuT      GAAA	SerAs       AGCGA	erg1	SDIL	. 7 :	
ATAA	aIleL	WalVa	GAG	ThrC	GT - Va	GAGAT	TAA	A - 1	CAAC	YLY GAA	nSei         AAG	TATC	Asp           GAT	GCT Ala	PAla      TGCC	yAsnG        CAACG	Mets ATGT		00
AGCG	ysA1a 	lGln       CCAA	YALA       GCA	sGLy        CGGI	IMet      GATG	   GAAGG	aLeuG	ACA	ICAC	ers	CTCA	CAGA	hrG1	roGl	hrII       CTAT	LuThr 	CTCAA		
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1464 base pairs
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPAX: 7377
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APPLICATION NUMBER: JP 106011/95
FILING DATE: 28-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Miller, Charles E.
REGISTRATION NUMBER: 24,576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 28-APR-1995 PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
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APPLICATION NUMBER:
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    144 GlnMetLysGluValGluAlaValValValAlaAlaLeuSerGlyLysSerSerGlySer 163
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                                                                    GluGluAlaSerLysSerMetGluSerThrLeuGluSerLeuGlnSerLeuSerAlaAla 143
                                                                                                                ThrSerThrProGlnGlyValProGlnGlnAspLysLeuSerGlyAsnGluThrLysGln 43
                                                                                                                                                                                                                                                                                                    GAAGAGGCGAGCAAAAGTATGGAGTCTACCTTAGAGTCACTTCAAAGCCTCAGTGCCGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UMBER: JP 106008/95
28-APR-1995
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Matches:
Conservative:
Mismatches:
Indels:
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483 1440	rGlnLysAlaThrLysLeuGlyAlaGlnTleLeuLysAlaTyrAlaAlaIle 		B 64
ωσ	PheThrGlnPheTrpGlnGlnAlaSerLysIleAlaSerLysGlnThrGlyGluSerAsn 		Qу
443 1320	4 ValAlaGlnPheGlnLySGluValGlyLySLeuGlnAlaAlaAlaAspMetIleSerMet		Qу Db
423 1260	euGlyLysGlyIleMetGlnMetGlnLeuSerGluMetGlnGlnAsn 		Qу
403 1200	rLysVall1LeSerSerLeuThrSerLysTrpValThrValGlyValGlyValValValVal 	38 114	Db Oy
383 1140	ysAsnPheProLysLeu             AGAACTTCCCCAAGCTC	36 108	pb Qy
363 1080	4 SerGlyIleLysAlaPheIleLysThrLeuValLysAlaIleAlaLysAlaIleSerLys 	2 4	ОУ
343 1020	AlaAlaValLys             CCGCTGTCAAA	32 96	Dp QA
323 960	4 AlaAlaAlaThrThrValAlaThrGlnIleThrValGlnAlaValValGlnAlaValLys 	30 90	dq Qy
303 900	aGlyLeuAlaAlaGlyAlaAlaValGlyAlaAlaAlaAlaGlyGlyAlaAlaGlyAla 	œ 4.	Ωу
283 840	4 SerValAlaIleThrValIleSerIleValAlaAlaIlePheThrCysGlyAlaGlyLeu 	26 78	Оу
263 780	IGlyThrmetAspThrValAsnThrValMetIleAlaVal 		Db Qy
243 720	/sGluArgGluGluTyrGlnGluMetLysAlaAlaGlu  -	6 2	Db Qy
223 660	uGlyLeuGlu          AGGTCTAGAA	20 60	dg Qy
203 600	4 GlulleGlyLeuAlaLeuAlaLysAlalleGlnThrLeuGlyGluAlaThrLysSerAla :	18 54	ФР
183 540	4 AlaLysLeuGluThrProGluLeuProLysProGlyValThrProArgSerGluValIle	16 48	ОУ
480	1 CAAATGAAAGAAGTCGAAGCGGTTGTTGTTGTTGCCTCCAGGGAAAAGTTCGGGTTCC	42	Db

RESULT 2 US-08-809-326A-17

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - nucleic search, using frame\_plus\_p2n model Run on January 27, 2003, 14:11:52; Search time 51 Seconds (without alignments) 2982.582 Million cell updates/sec

Title: Perfect score: US-09-889-314-2 2369

Sequence: 1 DTNMSISSSGPDNQKNIMS.....LKAYAAISGAIAGAHKTNNF 496

Scoring table: BLOSUM62 xyapop 10.0 , xyapext yyapop 10.0 , Yyapext ryapop 6.0 , Fyapext pelop 6.0 , Delext 0.5 7.0 7.0

441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Command line parameters:
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YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : 55432 Issued\_Patents\_NA:\* /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*
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is No. is the number of results predicted by chance to have greater than or equal to the score of the result being predicted by analysis of the total score distribution. printed,

## SUMMARIES

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55555 5555	97.8 97.8 54.1	Query Match I
1048 777 813 1296 1393 3622 3622 32768 46819	1464 1947 5658 5438	Query Match Length DB
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US-08-809-326A-7 US-08-809-326A-4 US-08-809-326A-18 US-08-81-079-9 US-08-591-079-7 US-08-591-079-7 US-08-961-527-71 US-08-961-527-72	US-08-809-326A-3 US-08-809-326A-17 US-08-809-326A-10 US-08-809-326A-25 US-08-809-326A-9	D
Sequence 7, Appli Sequence 4, Appli Sequence 18, Appli Sequence 9, Appli Sequence 7, Appli Sequence 71, Appl Sequence 72, Appl	Sequence 3, Appl. Sequence 17, Appl. Sequence 10, Appl. Sequence 25, Appl. Sequence 9, Appli.	Description
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US-08-146-930-1 US-08-458-240-1 PCT-US93-03993-1 US-08-961-527-377 5183745-1 US-08-669-785-1 5183745-5 US-09-702-251-3 US-09-702-251-3 US-09-206-942-64	US-09-134-001C-1685 US-08-669-785-3	PCT-US93-03993-1 US-09-134-001C-1515 US-09-134-001C-1626	US-08-591-079-5 US-08-146-930-1 US-08-458-240-1	US-08-961-527-368 US-08-961-527-370 US-08-961-527-372 US-08-961-527-373 US-08-961-527-373 US-09-103-840A-1 US-09-103-840A-2	US-08-961-527-363 US-08-961-527-364 US-08-961-527-364 US-08-961-527-365 US-08-961-527-365 US-08-591-079-1 US-08-591-079-1 US-08-591-079-1 US-08-961-527-369 US-09-453-7028-266 US-09-453-7028-263
Sequence 1, Appli Sequence 1, Appli Sequence 377, App Sequence 377, App Patent No. 5183745 Sequence 1, Appli Patent No. 5183745 Sequence 3, Appli Sequence 64, Appl	3,	Sequence 1, App. 15 Sequence 1515, Ap Sequence 1626, Ap	,,,,	368, 370, 372, 373, e 1, 7 e 2, 7	, , , , , , , , , , , , , , , , , , ,

## ALIGNMENTS

US-08-809-326A-3

Sequence 3, Application US/08809326A Patent No. 6165478 GENERAL INFORMATION: APPLICANT: OBATA, KAZUHIKO
APPLICANT: MATSUNOTO, AKITA
TITLE OF INVENTION: CHLAMYDIA
TITLE OF INVENTION: FUSED PROJ
TITLE OF INVENTION: CONTAINING
TITLE OF INVENTION: CONTAINING
TITLE OF INVENTION: OF ANTIBODY,
TITLE OF INVENTION: PREDMONIAL
TITLE OF INVENTION: PREDMONIAL
TITLE OF INVENTION: REAGENTS: I
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TITLE OF INVENTION: PREDMONIAL
TITLE OF INVENTION: PREDMONIAL APPLICANT: COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/809,326
FILING DATE: 19-MAR-1997 ZIP: 10036-2711 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk NUMBER OF SEQUENCES: 3: CORRESPONDENCE ADDRESS: PRIOR APPLICATION DATA: STREET: 1155 A CITY: New York STATE: New Yor COUNTRY: ADDRESSEE: CLASSIFICATION: New York 1155 Avenue of the Americas USA Izutsu, Hiroshi Pennie & Edmonds LLP CHLANTIDIA PNEUMONIAE ANTIGENIC POLYPEPTIDES, NAS CODING FUSED PROTEINS CONTAINING THE POLYPEPTIDES, DAAS CODING FUSED PROTEINS CONTAINING THE POLYPEPTIDES, TRANSFORMA THEREFOR, RECOMBINANT VECTORS, CARRYING THE DAAS, TRANSFORMA THEREFOR, METHOD AND REAGENTS FOR DETECTION AND/OR MEASUREM ANTIBODY, METHOD AND REAGENTS FOR DIAGNOSIS OF CHLAMYDIA OF ANTIBODY, METHOD AND ACENTS FOR DIAGNOSIS OF CHLAMYDIA PNEUMONIAE INFECTIONS, PROBES AND PRIMERS FOR DETECTION AND MEASUREMENT OF CHLAMYDIA PREUMONIAE GENE, AND METHOD AND REAGENTS FOR DETECTION AND/OR MEASUREMENT OF CHLAMYDIA REAGENTS FOR DETECTION AND/OR MEASUREMENT OF CHLAMYDIA PNEUMONIAE GENE. US/08/809,326A Version #1.30

301

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R;anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_elea.;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Accession: E88637
                                                                                                                                                                 RESULT
E70536
               R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; H. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
                                                                                 hypothetical protein Rv0804 - Mycobacterium tuberculosis (strain H37RV) C;Species: Mycobacterium tuberculosis C;Decies: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-C;Accession: E70536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-179 <570>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein AT4g19200 [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001 C;Accession: A85217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: E88637
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A; Residues: 1-178 <STO>
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C;Species: Caenorhabditis elegans
Rajandream, M.A.; Ro
Nature 393, 537-544,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: A85217
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Best Local
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8; Conser
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  Rogers,
44, 1998
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Pred. No.
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20;
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Search completed: January Job time: 53 secs

27,

2003,

16:37:07

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165 AGLAAGAA 172

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A;Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: E70536
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Molecule type: DNA
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A;Experimental source: GB:295618; GB:AL123456; NID:93261788; PIDN:CAB09107.1; PID:e31727
A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein AGR_C_4120 [imported] - Agrobacterium tumefaciens (strain C58, C;Species: Agrobacterium tumefaciens C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
                                                                                                                                                                                                                                     A; Title: Genome Sequence of the Plant Pathogen and A; Reference number: A97359; PMID:11743194 A; Accession: G97631
                                                                                                                                                                                                                                                                                           R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Science 294, 2323-2328, 2001
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Qy
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A; Residues: 1-214 <KUR>
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                                                                                                                             A; Gene:
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Best Local S
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284 AGLAAGAA 291
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8; Conserv
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                                                                                                            circular
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ilarity 100.0%;
Conservative
                                     Conservative
                                                                                                                                                                 GB:AE007869; PIDN:AAK88008.1;
                                                                                                            chromosome
                                                   100.0%;
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                                                     Score 8;
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23;
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R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J., M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans Rl. A;Ference number: A75250; MUID:20036896; PMID:10567266
A;Recession: H75262
A;Scatus: preliminary
A;Molecule type: DNA
A;Residues: 1-145 <WHI>A;Cross-references: GB:AE002082; GB:AE000513; NID:96460347; PIDN:AAF12073.1; PID:96460; A;Cross-references: GB:AE002082; GB:AE000513; NID:96460347; PIDN:AAF12073.1; A;Experimental source: Strain Rl
C;Genetics:
A;Gene: DR2529
A;Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H+-exporting ATPase (EC 3.6.3.6) lipid-binding protein - Neurospora crassa C:Species: Neurospora crassa C:Species: Neurospora crassa C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 03-Jun-2002 C:Accession: $43893 C:Accession: $43893 N.; Bowman, B.J.

MOI. Gen. Genet. 243, 82-90, 1994 A:Title: The proteolipid subunit of the Neurospora crassa vacuolar ATPase: isolation A:Reference number: $43893; MUID:94247360; PMID:8190074 A:Accession: $43893; MUID:94247360; PMID:8190074
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A;Status: preliminary
A;Malecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Rosidues: 1-161 <SIS>
A;Coss references: EMBL:L07105; NID:g168929; PIDN:AAA19974.1; PID:g168930
A;Coss references: EMBL:L07105; NID:g168929; PIDN:AAA19974.1; PID:g168930
A;Note: the authors translated the codon ATC for residue 63 as Tyr and GCT
C;Genetics:
A;Introns: 5/2; 9/3; 53/1; 141/1
A;Introns: 5/2; 9/3; 53/1; 141/1
C;Superfamily: vacuolar H+transporting ATPase 16K chain
C;Keywords: ATP; hydrolase
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N;Alternate names: vacuolar H+-transporting ATPase c-6
C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 03-Jun-2002
C;Accession: S32970; T38033
C;Accession: S32970; T38033
D: Movemen D: Collection D: Cohlogol D: Dhar D
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A;Cross-references: EMBL:x59947; NID:g5135; PIDN:CAA42572.1; PID:g5136 R;Murphy, L.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, V. submitted to the EMBL Data Library, August 1997 A;Reference number: Z21763
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Best Local S
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A; Residues: 1-161 <TOY>
                                                                                                                                                                                                                                   R; Toyama, R.; Goldstelr
Yeast 7, 989-991, 1991
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Best Local
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nes 8; Conser
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8; Conser
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Pred. No. 17;
0; Mismatches
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C.; Ma
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A; Accession: T38033
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-161 <MUR>
A; Cross-references: EMBL: Z98598; PIDN:CAB11240.1; GSPD
A; Experimental source: strain 972h-; cosmid clB3
C; Genetics:
A; Gene: SPACLB3.14
A; Map position: 1
A; Introns: 6/2; 8/2; 52/2; 160/3
C; Superfamily: vacuolar H+-transporting ATPase 16K cha
C; Keywords: ATP; hydrogen ion transport; hydrolase; me
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: mRNA
A;Residues: 1-165 <LALA;
A;Residues: 1-165 <LALA;
A;Cross-references: GB:M73232; NID:g166548; PIDN:AAA32712.1; PID:g166549
A;Cross-references: GB:M73232; NID:g166548; PIDN:AAA32712.1; PID:g166549
C;Keywords: ATP; hydrogen ion transport; hydrolase; transmembrane protein
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                                                                                                                                                                       R.Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Ko B.; Laub, M.T.; DeBoy, R.T.; Dodson, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: G87307
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                                                                                                           A;Molecule type: DNA
A;Residues: 1-178 <STO>
A;Cross-references: GB:AE005673; NID:g13421647; PIDN:AAK22459.1;
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                                                             A; Gene: CC0472
C; Superfamily:
                                                                                               C; Genetics:
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          Query Match
Best Local
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hes 8; Conserv
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8; Conserv
8; Conserv
                                                             ubiquinol-cytochrome-c reductase iron-sulfur pro
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                   Score 8; pred. No
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   core 8; DB 2;
Pred. No. 20;
Mismatches
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b. 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transmembrane protein
                                      Length 178;
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                                                                                                                             GSPDB: GN00148
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            Gaps
                                                                             Rieske [2Fe-2S]
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Conservative

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Indels

0;

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A;Molecule type: protein
A;Rosidues: 1-12, 'T', 14-18, 'TX', 21-33, 'X', 35-79, 'A', 81-111 <AMO>
A;Residues: 1-12, 'T', 14-18, 'TX', 21-33, 'X', 35-79, 'A', 81-111 <AMO>
A;Rote: Ser-98 is partially phosphorylated; this results in two slightly different C;Superfamily: rat acidic ribosomal protein P1
C;Keywords: phosphoprotein; protein biosynthesis; ribosome
F;1-111/Product: ribosomal protein Lile! #status experimental <MAT>
F;98/Binding site: phosphate (Ser) (covalent) (partial) #status experimental
                                                                          A;Cross-references: EMBL:X65065; NID:g10633; PIDN:CAA46198.1; PID:g10634 A;Note: it is uncertain whether Met-1 or Met-3 is the initiator C;Superfamily: rat acidic ribosomal protein P1 C;Keywords: phosphoprotein; protein biosynthesis; ribosome
                                                                                                                                                                                      R;Vazquez, M.P.; Schijman, A.G.; Panebra, A.; Levin, M.J. nucleic Acids Res. 20, 2893, 1992
A;Title: Nucleotide sequence of a cDNA encoding another Trypanosoma A;Reference number: S22950; MUID:92310999; PMID:1614880
A;Accession: S22950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Keywords: protein biosynthesis; ribosome F;1-111/Product: acidic ribosomal protein P2.e.B F;70-89/Region: alanine-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acidic ribosomal protein P2 - fungus (Cladosporium herbarum)
C;Species: Cladosporium herbarum
C;Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_cha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 В
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A;Title: The primary structure of ribosomal protein eL12/eL12-P from Artemia salina A;Reference number: A02775; MUID:80004136; PMID:477981
A;Accession: A02775
                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-112 < VAZ>
                                                                                                                                                                                                                                                                                           C;Species: Trypanosoma cruzi
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change
C;Accession: S22950; S19948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-111 <ZHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted to the EMBL Data Library, A;Description: A cDNA clone coding A;Reference number: S41866 A;Accession: S41866
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession:
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                                                                                                                                                                                                                                                                                                                                                 acidic ribosomal protein P2-B - Trypanosoma cruzi
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Best Local S
Matches 8
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  Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acid/glutamic acid-rich
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100.0%; Pred. No.
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    0;
                    Score 8;
Pred. No.
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                      DB 1;
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G70354
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C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
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hypothetical protein - Deinococcus radiodurans (strain C;Speciles: Deinococcus radiodurans C;Speciles: Deinococcus radiodurans C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #tex C;Accession: H75262
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                                                                                                                                                                                                                                                                                                                                                                                                           A; Residues: 1-143 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: A82950; A; Accession: A83149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           adman, S.; Yuan, Y.; Brody, .; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Stover, C.K.; Pham, X.Q.; adman, S.; Yuan, Y.; Brody,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession: A83149
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                                                                              H75262
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Conservative
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Mismatches
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Gaps

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Length 143;

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A;Title: The complete genome of the hyperthermophilic bacterium A;Reference number: A70300; MUID:98196666; PMID:9537320 A;Accession: G70354
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A;Residues: 1-132 <AQF>
A;Cross-references: GB:AE000698; NID:g2983224; PIDN:AAC06830.1;
A;Experimental source: strain VF5
A; Title: Complete genome sequence of Pseudomonas aeruginosa PA01, A; Reference number: A82950; MUID: 20437337; PMID: 10984043
                                                                                                                                                                                              C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 01-Mar-2002
                                                                                                                                                                                                                     hypothetical protein PA3971 [imported] - Pseudomonas aeruginosa C; Species: Pseudomonas aeruginosa
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                                                                                                            Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-May-1998
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submitted to the EMBL Data Library, November 1998
submitted to the EMBL Data Library, November 1998
A; Reference number: Z25985
A; Accession: T52147
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-106 <TAY>
A; Cross-references: EMBL: AL033497; PIDN: CAA21967.1
A; Cross-references: EMBL: AL033497; PIDN: CAA21967.1
A; Experimental source: strain 1161; cosmid Ca49C10
C; Genetics:
                                                                                                                    A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-10 <BEL2>
A; Residues: 1-10 <BEL2>
A; Residues: 1-10 <BEL2>
A; Residues: 1-10 <BEL2>
A; Cross-references: GB: Y000466; NID: 95064; PIDN:CAAA68528.1; PID: 95065
A; Cross-references: J100, T.
R; Otaka, E; Higo, K.I.; Itoh, T.
R; Otaka, E; Higo, K.I.; Itoh, T.
R; Class, E; Liposomal proteins: VII. Cytoplasmic ribosomal proteins from: A; Title: Yeast ribosomal proteins: VII. Cytoplasmic ribosomal proteins from: A; Reference number: S07293; MUID:84038947; PMID:6355773
A; Reference number: S07293; MUID:84038947; PMID:6355773
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Residues: 1-15, M; 1-21, M; 23, 'Z', 25-32,'Z', 34, 'ZXZ', 38-39, 'Z' <OTA>
A; Molecule type: protein
A; Molecule type: protein
A; Reinhardt, R; Lyne, M.; Rajandream, M.A.; Barrell, B.G.
R; Beck, A.; Reinhardt, R; Lyne, M.; Rajandream, M.A.; Barrell, B.G.
B; Beck, A.; Reinhardt, R; Lyne, M.; Rajandream, M.A.; Barrell, B.G.
A; Reinhard; translated from GB/EMBL/DDBJ
A; Mccession: T40800
A; Mccession: T40800
A; McCession: T40800
A; McCession: T40800
A; McCession: T40800
A; McCession: T40800
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A; Map position: 1
C; Superfamily: ra
C; Keywords: prote
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C;Species: Schizosaccharomyces pombe
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 10-Dec-1999
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 10-Dec-1999
C;Accession: B34715; A27304; S10054; T40800
C;Accession: B34715; A27304; S10054; T40800
R;Beltrame, M.; Bianchi, M.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mol. Cell. Biol. 10, 2341-2348, 1990
A;Title: A gene family for acidic ribosomal proteins in A;Reference number: A34715; MUID:90220620; PMID:2325655
A;Accession: B34715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60s acidic ribosomal protein P2.2 - fission yeast (Schizosaccharomyces pombe) N.Alternate names: acidic ribosomal protein 2; ribosomal protein SP-L40c; ribo
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A; Residues: 1-110 <BEL1>
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Best Local
A; Molecule type: DNA
A; Residues: 1-110 <BEC>
A; Cross-references: EMBL: AL032684;
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pred. No.
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                             PIDN:CAA21791.1; GSPDB:GN00067;
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A; Experimental source: strain 972h-; clone pl p8B7 C; Genetics:
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A;Introns: 103/3
A;Introns: 103/3
C;Superfamily: rat acidic ribosomal protein Pl
C;Superfamily: rat acidic ribosomal biosynthesis; ribosome
C;Keywords: phosphoprotein: protein biosynthesis; ribosome
F;1-110/Product: acidic ribosomal protein P2.2 #status expe
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C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 10-Dec-1999
C;Accession: D34715; T39961_
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A;Title: A gene family for acidic ribosomal proteins in
A;Title: A gene family for acidic ribosomal proteins in
A;Reference number: A34715; MUID:90220620; PMID:2325655
A;Recession: D34715
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A;Residues: 1-110 <XIA>
A;Cross-references: EMBL.AL035065; PIDN:CAA22631.1;
A;Experimental source: strain 972h-; cosmid c2367
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A; Residues: 1-110 <BEL>
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A;Introns: 103/3
C;Superfamily: rat acidic ribosomal
C;Keywords: phosphoprotein; protein
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Best Local !
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                                                                                                                                                     ribosomal protein L12eI - brine shrimp
N;Alternate names: ribosomal protein eL12
C;Species: Artemia salina (brine shrimp)
C;Date: 30-Nov-1979 #sequence_revision 31-Mar-1992 #text_change 22-Jun-1999
C;Accession: A25208; A02775
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                                                                                           R;Maassen, J.A.; Schop, E.N.; Brands, J.H.G.M.; Van Hemert, F.J.; Lenstra, J.A.; Moll
Eur. J. Biochem. 149, 609-616, 1985
A;Title: Molecular cloning and analysis of cDNA sequences for two ribosomal proteins
                                  A; Reference number: A91146;
A; Accession: A25208
A; Molecule type: mRNA
A; Residues: 1-108 <MAA>
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Best Local 9
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les 8; Conserv
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                                                                    MUID:85230659; PMID:3839187
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Mismatches
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o. 13;
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A;Molecule type: DNA
A;Residues: 1-1616 <COL>
A;Residues: 1-1616 <COL>
A;Cross-references: GB:Z83858; GB:AL123456; NID:g3261675; PIDN:CAB06103.1; PID:g1781167
A;Experimental source: strain H37Rv
R;Smith, D.R.; Robison, K.
submitted to the EMBL Data Library, September 1994
A;Description: Mycobacterium tuberculosis cosmid tbc2.
A;Reference number: S73053
A;Accession: S73075
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A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: G70668
hypothetical protein W06A7.3a - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #te
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A;Residues: 'MMGARWPVARCLSTEL',48-917,'RSEARSRRGCGMSGRAAPPAPPIGPPIGIP','PMPPIIPVEPAGPVFN
A;Cross-references: EMBL:U00024; NID:g560506; PIDN:AAA50928.1; PID:g560507
                                                                   T26215
                                                                                                                                                                                                                                                                                                                          A; Introns: 1827/1; 1866/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: A; Accession: T26216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, August 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R; Ainscough,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                 A; Map position:
                                                                                                                                                                                                                                                                                                                                                                     A; Gene: CESP:W06A7.3c
                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 1-2484 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary; translated from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S. Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. ajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Keywords: carrier protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Superfamily: Mycobacterium tuberculosis probable polyketide synthase pksl; acyl carri
                                                                                                                                                                                                                                                                                                                                                                                            Genetics:
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Best Local
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                                                                                                                                                      GAAVGAAAA 2215
                                                                                                                                                                                                                                       Similarity 9; Conserv
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9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [acyl-carrier-protein] S-malonyltransferase homology
in: short-chain alcohol dehydrogenase homology <SADH>
in: acyl carrier protein homology <ACP1>
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  #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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100.0%; Pr
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100.0%; Pred. N
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                                                                                                                                                                                                                                                              DB 2;
5. 25;
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                                                                                                                                                                                                                                         0,
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R; Sezutsu, H.; Tamura, T.; Yukuhiro, K.
submitted to the EMBL Data Library, August 1998
A; Description: Characterization of the full length fibroin
A; Reference number: Z20995
A; Accession: T31328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: T26215
R;Ainscough, R.
                                                                                                                                                                                                    R;Murphy, L.; Harris, D.; Parkhill, submitted to the EMBL Data Library, A;Reference number: Z21548
A;Accession: T35731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Map position: 5
A; Introns: 1827/1; 1866/3;
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Query Match
Best Local Similarity
Thes 8; Conserve
                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-81 <MUR>
A; Cross-references: EM
                                                                                                                                                                                       A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                              C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999 C;Accession: T35731
                                                                                                                                                                                                                                                                                                                 hypothetical protein SC7H1.36c SC7H1.36c - Streptomyces coelicolor (fragment) C; Species: Streptomyces coelicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Introns:
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A; Residues: 1-2639 <SEZ>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Antheraea pernyi (Chinese oak silkmoth)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999
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A; Residues: 1-2607 <WIL>
                                                                                    A; Gene:
                                                                                                                     A; Experimental source: strain A3(2)
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9; Conserv
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the EMBL Data Library, January 1998
 1.6%; Score 8; illarity 100.0%; Pred. No. Conservative 0: Min-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.8%;
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100.0%; Pred. No. 26
Live 0; Mismatches
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Pred. No.
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red. No. 26;
Mismatches
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                                               Length 81;
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                                                                                                                                         SCOEDB: SC7H1.36c
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Mismatches

0;

Indels

0,

Gaps

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sarcosine oxidase (EC 1.5.3.1) alpha chain [validated] - Corynebacterium sp. C;Species: Corynebacterium sp. C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 26-May-2000 C;Date: 14-869 #sequence_revision 16-Aug-1996 #text_change 26-May-2000 C;Date: 140889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;28-860/Product: elastin #status predicted <MAT>F;850-855/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R.Chlumsky, L.J.; Zhang, L.; Jorns, M.S.
J. Biol. Chem. 270, 18252-18259, 1995

A.Title: Sequence analysis of sarcosine oxidase and nearby genes reveals homologies with A.Title: Sequence number: A57385; MUID:95355441; PMID:7543100

A.Reference number: A57385; MUID:95355441; PMID:7543100

A.Recession: I40889

A.Status: preliminary; translated from GB/EMBL/DDBJ

A.HOLOCULE type: DNA

A.HOLOCULE type: DNA

A.Residues: 1-967 <RES>
A.Cross-references: EMBL:U23955; NID:g927587; PIDN:AAC43461.1; PID:g927591

C.Genetics:
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                                                                                                                                                                                                                                                                                                 potassium channel protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C;Accession: T18807
C;Accession: T18807
R;Goldstein, S.A.; Price, L.A.; Rosenthal, D.N.; Pausch, M.H.
Proc. Natl. Acad. Sci. U.S.A. 93, 13256-13261, 1996
proc. Natl. Acad. Sci. U.S.A. 93, 13256-13261, 1996
A;Title: ORK1, a potassium-selective leak channel with two pore domains clon
A;Reference number: Z17770; MUID:97075152; PMID:8917578
A;Accession: T13807
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A;Molecule type: mRNA
A;Residues: 1-1001 <COL>
A;Cross-references: EMBL:U55321; N
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                                20
                                                                                                                                                   A; Map position:
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les 9; Conserv
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nes 9; Conserv
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                                       294 AAAAGGAAG 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGAAGAAAA 121
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    AAAAGGAAG
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9; Conserv
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ilarity 100.0%;
Conservative (
                                                                            Conservative
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                                                                                                                                                                          FlyBase:FBgn0017561
        772
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                                                                              1.0.0%; F
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Pred. No.
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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon R;Cole, S.T.; Brosch, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
Nature 393, 537-544, 1998
A;Authors: Squres, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Authors: Deciphering the biology of Mycobacterium tuberculosis from the complete geno A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Recession: B70985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable polyketide synthase - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Datc: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 26-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-1017 <COL>
A;Cross references: GB:Z95617; GB:AL123456; NID:g3242249; PIDN:CAB09100.1; PID:e31726
A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dve protein - 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:AB010299; NID:g3523072; PIDN:BAA32660.1; PID:g3523073
A;Experimental source: strain Oregon R
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: A novel homeobox gene mediates the Dpp signal t A;Reference number: Z14112; MUID:98402482; PMID:9732270 A;Accession: T00117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dve protein - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 22-Jan.1999 #sequence_revision 22-Jan-1999 #text_change 17-Nov-2000
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T00117
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R; Nakagoshi, H.; Hos
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polyketide synthase pks1 - Mycobacterium tuberculosis
N;Alternate names: polyketide synthase pks002c
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #te
C;Accession: G70668; S73075
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A; Residues: 1-1019 <NAK>
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#text\_change

20-Jun-2000

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A:Residues: 1,'RS',4-11,'E',13-225,260-636,'V',638-747 <RA3>A:Cross-references: GB:K03506; NID:g163027; PIDN:AAA30506.1; R:Cicila, G.; May, M.; Ornstein-Goldstein, N.; Indik, Z.; Mor Biochemistry 24, 3075-3080, 1985
A:Title: Structure of the 3' portion of the bovine elastin ge A:Reference number: A22343; MUID:85280426; PMID:2992576
A:A:Accession: A22343
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Blochemistry 28, 2365-2370, 1989
A;Title: Structure of the bovine elastin gene and SI nuclease analysis of alternative a.Reference number: A31865; MUID:89274159; PMID:2543440
                                                                                                                    R;Brown, P.L.; Mecham, L.; Tisdale, C.; Mecham, R.P. Biochem. Biophys. Res. Commun. 186, 549-555, 1992 A;Title: The cysteine residues in the carboxy terminal domain A;Reference number: A58621; MUID:92337651; PMID:1632791 A;Contents: annotation, disulfide bonds
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A;Residues: 678-683,685-747 <ROS>
A;Residues: 678-683,685-747 <ROS>
A;Cross-references: GB:M31898; NID:g163015; PIDN:AAA96417.1;
A;Cross-references: GB:M31898; NID:g163015; PIDN:AAA96417.1;
R;Brown, P.L.; Mecham, L.; Tisdale, C.; Mecham, R.P.
R;Brown, P.L.; Mecham, L.; Tisdale, C.; Mecham, R.P.
                                                                                                                                                                                                                                                                                                                                             R;Rosenbloom, J.
Lab. Invest. 51, 605-623, 1984
A;Title: Biology of disease: Elastin: Relation of protein A;Reference number: I45885; MUID:85059254; PMID:6150137
A;Accession: I45886
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A; Residues: 1, 'RS', 4-11,'E',13-636,'V',638-747 <RAJ>
A; Cross-references: GB:J02717; NID:g163019; PIDN:AAA30503.1;
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A; Title: Primary structures of bovine elastin a, b, and A; Reference number: A92640; MUID:87194772; PMID:3032943
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                                                                                               C; Comment: The term tropoelastin
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A; Residues: 1, 'RS', 4-11, 'E', 13-225, 240-636, 'V', 638-747 <RA2>
A; Cross-references: GB:K03505; NID:g163025; PIDN:AAA30505.1;
A; Accession: C26728
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J. Biol. Chem. 262, 5755-5762, 1987
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A; Residues: 1-27 < YEH>
                            A; Introns: 634/3;
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A; Residues: 613-747
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                                                                        ine oxidase activity.
                                                                                                                                                                                                                                                                                                                      A; Status: preliminary; translated from GB/EMBL/DDBJ
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;Date: 08-Jun-1989 #sequence_revision 26-Jul-1996 #text_change 22-Jun-1999
;Accession: A31865; A26728; B26728; C26728; A22343; I45886
;Yeh, H.; Anderson, N.; Ornstein-Goldstein, N.; Bashir, M.M.; Rosenbloom, J.C.; iochemistry 28, 2365-2370, 1989
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653/3; 676/3; 689/3; 707/3; 716/3; 733/3 of introns is incomplete
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A;Map position: 5
C;Superfamily: elastin
C;Keywords: alternative splicing; extracellular matrix;
F;1-27/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                 C;Accession: A55721
R;Wydner, K.S.; Sechler, J.L.; Boyd, C.D.; Passmore, H.C.
Genomics 23, 125-131, 1994
A;Title: Use of an intron length polymorphism to localize
A;Reference number: A55721; MUID:95130069; PMID:7829060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 655-669,671-716,732-770 <YOO>
C; Superfamily: elastin
C; Keywords: alternative splicing; extracellular matrix;
F;760-765/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Yoon, K.; Davidson, J.M.; Boyd, C.; May, M.; LuValle, P.; Ornstein-Goldstein, Arch. Biochem. Biophys. 241, 684-691, 1985
A;Title: Analysis of the 3' region of the sheep elastin gene.
A;Reference number: A24758; MUID:85305763; PMID:3839997
A;Accession: A24758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R; Mauch, J.C.; Sa
Matrix Biol. 14,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession:
R; Mauch, J.C.
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F;27-747/Product: elastin #status predicted <MAT>
F;105,109,252,271,275,324,327,400,404,407,445,448,489,493,544,548,552,606,609,645,649
                                                                                                                                                                                                                                                                                        N;Alternate names: tropoelastin
C;Species: Mus musculus (house mouse)
C;Date: 18-Aug-1995 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Ovis orientalis aries, Ovis C;Date: 23-Aug-1996 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;1-747/Product: elastin precursor, splice form a *status predicted <EPA>F;1-225,260-747/Product: elastin precursor, splice form c *status predicted F;1-225,240-747/Product: elastin precursor, splice form b *status predicted
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                                                                                                            A; Molecule type: mRNA
A; Residues: 1-860 <WYD>
A; Cross-references: GB:U08210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;737-742/Disulfide bonds: #status experimental
                                                                                         A;Cross-references:
C;Genetics:
                                                                                                                                                                           A; Accession: A55721
                                                                                                                                                                                                                                                                                                                                                         elastin precursor -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Title: Extensive alternate exon usage at the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                298
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1, 635-641, 1994
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; Mismatches
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13-Mar-1997
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                                                                                                              PIDN: AAA80155.1;
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#text_change 24-Oct-1997
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                                                                                                              PID: 9473274
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glycoprotein; hydroxylysine

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C;Genetics:
A;Gene: SCOEDB::
C;Superfamily:
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C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 08-Sep-2000
C;Accession: T34870
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T34870
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submitted to the EMBL Data
A; Reference number: Z21560
A; Accession: T34870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                secretion protein, HlyD family [imported] - Agrobacterium tumefaciens (strain C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002 C;Accession: AE2972 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, C.; Chen,
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AE2972
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A;Reference number: AB2577; PMID:11743193
A;Accession: AE2972
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Karp, P.; Romero, P.; Zhang, S.; Science 294, 2317-2323, 2001
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A;Map position
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Similarity 100.0%;
9; Conservative (
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st 1999
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RESULT

A; Molecule type: DNA A; Residues: 1-491 <TET> A; Cross-references:

GB:AE002353; GB:AE002160; NID:97190891; PIDN:AAF39663.1; PID:9719

pneumoniae AR39

A; Status: preliminary

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C; Accession: F98310
C; Accession: F98310
R; Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N
R; Goodner, B.; Wollam, C.; Allinger, M.; Doughty,
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A;Title: Genome Sequence of the Plant Pathogen and
A;Reference number: A97359; PMID:11743194
A;Accession: F98310
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A; Residues: 1-474 <KUR>
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Conserved hypothetical protein TC0867 [imported] - Chlamydia muridarum (strain conserved hypothetical protein TC0867 [imported] - Chlamydia muridarum (strain conserved hypothetical protein TC0867 [imported] - Chlamydia muridarum (strain conserved hypothetical protein TC0867 [imported] - Chlamydia muridarum (strain conserved hypothetical protein TC087 [imported] - Chlamydia muridarum (strain conserved hypothetical protein TC0867 [imported] - Chlamydia preumoniae hypothetical protein conserved hypothetical protein TC0867 [imported] - Chlamydia preumoniae hypothetical protein conserved hypothetical protein TC0867 [imported] - Chlamydia preumoniae hypothetical protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein prote
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Science 294, 2323-2328, 2001
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A;Residues: 1-407 <ARN>
A;Cross-references: GB:AE001328; GB:AE001273; NID:g3329015; PIDN:AAC68180.1;
A;Experimental source: serotype D, strain UW-3/Cx
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A; Gene: CT578
C; Superfamily: conserved
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Best Local S
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; Scott, C.; Lap
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Markelz,
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Salzbe
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RESULT 7
T49895
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C;Superfamily: peripheral
C;Keywords: mitochondrion
                                                                                                                                                                                                                                                 Gene 155, 201-205, 1995

A:Title: Comparison of repetitive elements in the third A:Reference number: 138724; MUID:95237610; PMID:7721091
A:Accession: 138724
A:Status: preliminary; translated from GB/FMRI./DDBI
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C:Date: 02-Jun-2000 #sequence_revision
C:Accession: T49895
                             δõ
                                                                                                                                                                                                                                                                                                              mitochondrial benzodiazepine receptor - human C;Specles: Homo sapiens (man) C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change C;Accession: I38724
R;Yakovlev, A.G.; Ruffo, M.; Jurka, J.; Krueger, K.E. Gene 155, 201-205, 1995
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Best Local Similarity
"---has 9; Conserv:
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submitted to the Protein Sequence Dat
A:Reference number: Z24493
A;Accession: T49895
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A;Cross-references: EMBL:X78223; NID:g467626; PIDN:CAA55067.1; C;Superfamily: rat acidic ribosomal protein P1
멍
                                                                                                                                                                       C;Genetics:
A;Gene: MBR
                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-169 <RES>
A; Cross-references: EMB
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A; Molecule type: DNA
A; Residues: 1-153 <BEV>
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A;Experimental source: cultivar Columbia; BAC clone T211
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                                                                           Query Match
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evision 02-Jun-2000 #text_change 17-Nov-2000
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C;Accession: 138105

C;Accession: 138105

C;Accession: V.J.; Strauss, J.F.; Miller, W.L.

Genomics 18, 643-650, 1993

A;Title: The human peripheral benzodiazepine receptor gene: A;Reference number: A49361; MUID:94140364; PMID:8307574

A;Accession: I38105
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C;Superfamily: peripheral-type benzodiazepine receptor
C;Keywords: mitochondrion; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eur. J. Biochem. 195, 305-311, 1991
A;Title: Molecular cloning and chromosomal localization A;Reference number: S14257; MUID:91146565; PMID:1847678
A;Accession: S14257
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S14257
                                                                         R;Xu, G.H.; Hu, B.R.; Luo, C.Q.; Chen, R.Z.; Qiu, P.X. Chinese Blochem. J. 13, 423-427, 1997
A;Title: Cloning of the cDNAs encoding human periphera
                                                                                                                                  C; Species: Homo sapiens (man)
C; Date: 10-Jul-1998 #sequence
C; Accession: JE0149
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C; Superfamily:
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C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change
C;Accession: I38105
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A;Residues: 1-169 <RIO>
A;Cross-references: GB:M36035; NID:g184333;
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A; Molecule type: n
A; Residues: 1-169
                                    A; Reference number: A; Accession: JE0149
                                                                                                                                                                         peripheral benzodaizepine receptor - human
C; Species: Homo sapiens (man)
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A;Cross-references: GDB:127347; OMIM:109610
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R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138. A;Reference number: A86491; MUID:20330349; PMID:10871362
A;Accession: G85591
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(B86591

C.TS78 hypothetical protein [imported] - Chlamydophila pneumoniae (strain J138)

C.TS78 hypothetical protein [imported] - Chlamydophila pneumoniae

C.Species: Chlamydophila pneumoniae, Chlamydia pneumoniae

C.Paccession: G86591

C.Paccession: G86591

C.Paccession: G86591
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C; Superfamily:
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A; Residues: 1-488 <STO>
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female sterile homeotic protein, 205K - fruit fly (Drosophila N;Alternate names: membrane protein fsh, 205K N;Contains: female sterile homeotic protein, 110K C:Species: Drosophila melanogaster C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_chang C;Accession: A43742; B43742
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R;Haynes, S.R.; Mozer, B.A.; Bhatia-Dey, N.; Dawid, I.B Dev. Biol. 134, 246-257, 1989
A;Title: The Drosophila fsh locus, a maternal effect ho A;Reference number: A43742; MUID:89276730; PMID:2567251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: FlyBase:FBgn0004656
A;Cross-references: FlyBase:FBgn0004656
C;Superfamily: unassigned bromodomain proteins; bromodomain homo
C;Keywords: alternative splicing; transmembrane protein
F;1-2038/product: female sterile homeotic protein, 205K #status
F;1-1106/product: female sterile homeotic protein, 110K #status
F;59-116/Domain: bromodomain homology <BR01>
F;503-560/Domain: bromodomain homology <BR02>
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A; Residues: 1-2038 <HAY>
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A; Residues: 1-1106 <HA2>
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                                                                                                                                                                                            A;Title: Genome sequence of a huma A;Reference number: Z20876; MUID:9 A;Accession: T30714 A;Status: preliminary; translated A;Molecule type: DNA A;Residues: 1-128 <SEND
                                                                                                                                                                                                                                                                                                                                                      hypothetical protein 112L - Molluscum contagiosum virus 1
N;Alternate names: MC112L
C;Species: Molluscum contagiosum virus 1
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jul-2000
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C;Genetics:
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R;Achatz, G.; Oberkofler, H.; Simon, B.; Lechenauer, E.; Ouger, A.; Namore, B.; Submitted to the EMBL Data Library, March 1994
A;Description: Molecular characterization of allergens of Cladosporium herbarum A;Reference number: \$43108
A;Accession: \$43115
A;Molecule type: mRNA

Oberkofler, H.; Simon, B.; Lechenauer, E.; Unger, A.; Kandler,

acidic ribosomal protein P2 - fungus (Cladosporium herbarum)
C;Species: Cladosporium herbarum
C;Date: 19-Mar-1997 #sequence\_revision 06-Jun-1997 #text\_cha
C;Accession: S43115

#text\_change 13-Aug-1999

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A;Title: Comparative genomes of Clamydia pneumonlae and C. trachomatis.
A;Reference number: A72000; MUID:99206806; PMID:10192388
A;Accession: F72031
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-493 <ARN>
A;Cross-references: GB:AE001662; GB:AE001363; NID:g4377118; PIDN:AAD18947.1; PID:g437712
A;Experimental source: strain CWL029
C;Genetics: A;Gene: CPn0809
C;Superfamily: conserved hypothetical protein TC0867
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A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39 A;Reference number: A81500; MUID:20150255; PMID:10684935
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B97297
T01579
E96573
S74886
AG2103
C84362
I56542
AC1323
AD1694
H89152
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C83109
H71857
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                                                                              C86744
G70545
T03925
T03933
JC5803
JC7155
S75075
S750713
A36068
S44876
T213699
A70896
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OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OREGON R;
RA Nakagoshi H., Hoshi M., Nabeshima Y., Matsuzaki F.;
RA Nakagoshi H., Hoshi M., Nabeshima Y., Matsuzaki F.;
RA Nakagoshi H., Hoshi M., Nabeshima Y., Matsuzaki F.;
RR EMBL; ABO10299; BA32560.1; -.
DR PSECTICITY Within target cells.";
RL Genes Dev. 0.0-0(1998).
DR EMBL; ABO10299; BA32560.1; -.
DR HSSP; P10037; AUJ7.
DR HSSP; P10037; AUJ7.
DR HSSP; F10037; AUJ7.
DR HSSP; F10038; HOX; 2.
DR F1yBase; FB900046; homeobox.
DR F1yBase; FB900046; homeobox.
DR SMART; SM001389; HOX; 2.
DR SMART; SM00389; HOX; 2.
DR SMSTTE; PS50071; HOMEOBOX.2; 2.
DR PROSITE; PS50071; HOMEOBOX.2; 2.
DR PROSITE; PS50071; HOMEOBOX.2; 2.
DR SEQUENCE 1019 AA; 111355 MW; 5D22A104A0D0FOCC CRC64;
SEQUENCE 1019 AA; 111355 MW; 5D22A104A0D0FOCC CRC64;
SEQUENCE 1019 AA; 111355 MW; 5D22A104A0D0FOCC CRC64;
SEQUENCE 1019 AA; 111355 MW; 5D22A104A0D0FOCC CRC64;
SEQUENCE 1019 AA; 111355 MW; 5D22A104A0D0FOCC CRC64;
SEQUENCE 1019 AA; 111355 MW; 5D22A104A0D0FOCC CRC64;
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SEQUENCE 1019 AA; 111355 MW; 5D22A104A0D0FOCC CRC64;
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SEQUENCE 1019 AA; 111355 MW; 5D22A104A0D0FOCC CRC64;
SEQUENCE 1019 AA; 111355 MW; 5D22A104A0D0FOCC CRC64;
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Q960M0;
Q960M0;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence upd
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation upd
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation upd
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation upd
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InterPro; IPR001257; Chitinase_18/2.
InterPro; IPR001257; Chitinase_18/2.
InterPro; IPR001253; Glyco_hydro_18.
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                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF01607; CBM_14; 1.

Pfam; PF00704; Glyco_hydro_18; 2.

ProDom; PD000471; Glyco_hydro_18; 2.

PROSITE; PS01095; CHITINASE_18; UNKNOWN_2.

SEQUENCE 1013 AA; 113285 MW; 266981AD0685EC02
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NCBI_TaxID=1773;
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PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_1.
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Diptera; Brachycera; Musc
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01-NOV-1998
01-JUN-2002
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
101-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 106.4 kDa protein (Polyketide synthase).
PKS9 OR RV1664 OR MTCY275.03 OR MT1704.
Mycobacterium tuberculosis.
Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003880; PROTTE ATTACH.

Pfam; PF00698; Acyl_transf; 1.

Pfam; PF00109; ketoacyl-synt; 1.

Pfam; PF02801; ketoacyl-synt; 1.

Pfam; PF00550; pp-binding; 1.

PROSITE; PS0075; ACP_DOMAIN; 1.

PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.

PROSITE; PS00012; PHOSPHOPANTETHEINE; Complete SEQUENCE 1017 AA; 106402 MW; B93A22D8818AE0EC (SEQUENCE 1017 AA); 106402 MW; B93A2ZD8818AE0EC (SEQUENCE 1017 AA); 106402 MW; B93AZDB818AE0EC (SEQUENCE 1017 AA); 106402 MW; B
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STRAIN=CDC 1551 /
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                             DVE OR CG5799
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InterPro; IPR001227;
InterPro; IPR000794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (APR-2001) to EMBL; Z95617; CAB09100
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Drosophila melanogaster (Fruit fly)
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P25715; 1MLA.
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393:537-544(1998).
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9; Conser
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8 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                     486
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Ketoacyl-synt.
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Mycobacteriaceae; Mycobacterium.
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Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; endicotyledons; core eudicots; Roside eurosids II; Brassicales; Brassicaceae; Arabidopsis.

MCBI_TaxID-3702;
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TAC and E
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
                                                                                                                                                                                   Oryza sativa (Rice), and Oryza sativa (Rice), and Oryza sativa (japonica cultivar-group). Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryza. NCBI_TaxID=4530, 39947;
                                                                                                                                                                                                                                                                                                                                                                                OBWON1;

01-MAR-2002 (TrEMBLrel. 20, Created)

01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

Hypothetical 82.1 kDa protein.

P0681B11.1 OR B1085F01.16.
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InterPro; IPR000205; NAD_binding.
Pfam; PF01593; Amino_oxidase; 1.
SEQUENCE 746 AA; 82350 MW; EOFD
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SEQUENCE FROM N.A.
STRAIN=CV. NIPPONBARE;
SASAKI T., MATSUMOTO T., YAMAN
"OTYZA SATIVA NIPPONBATE(GA3)
clone:P0681B11.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CM0M1
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Res. 7:217-221(2000).
; AP001307; BAB01917.1;
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EMBL/GenBank/DDBJ data
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EMBL; AP003302; BAB78635.1; -
EMBL; AP003330; BAB8980:1; -
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR0002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF00069; pkinase; I
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SMART; SM00220; S_TK; 1.
SMART; SM002219; TyTK; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM;
PROSITE; PS00109; PROTEIN_KINASE_TYR;
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SEQUENCE
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Mammalia; Eutheria;
NCBI_TaxID=10090;
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01-MAR-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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SEQUENCE 748 AA; 8
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Q1-NOV-1996 (TrEMBLrel. 01,
Q1-NOV-1996 (TrEMBLrel. 01,
Q1-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AF289665; AAF99336.1; -. InterPro; IPR001899; Gram_pos_anchor. PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
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Mycobacterium tuberculosis.
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Q91TN6
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q91TN6;
Q91TN6;
Q1-DEC-2001
Q1-DEC-2001
Q1-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q99K82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel 17, Created)
01-JUN-2001 (TrEMBLrel 17, Last sequence update)
01-DEC-2001 (TrEMBLrel 19, Last annotation update)
Similar to hypothetical protein.
Mus musculus (Mouse)
                                           Darai G., Bahr U.; Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases EMBL, AF281817; AAK57101.1; -. InterPro; IPR002597; Herpes_env.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAR-2001) to the EMBL/GenBa
EMBL; BC004831; AAH04831.1; -.
InterPro; IPR000759; Adrndx_reductase
InterPro; IPR002937; Amino_oxidase.
InterPro; IPR000205; NAD_binding.
Pfam; PF01593; Amino_oxidase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
Submitted (MAR-2001)
SEQUENCE
                              InterPro; IPR0
Pfam; PF01673;
                                                                                                                                                                                         STRAIN=2;
                                                                                                                                                                                                                          SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                         Shrew) Herpesvirus."
                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21211637;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tupaia herpesvirus.
Viruses; dsDNA viruses,
Betaherpesvirinae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical
SEQUENCE 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00419; ADXRDTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                       Bahr U., Darai G.;
"Analysis and Characterization of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          280
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                                                                                                                                                                                                                                                                                          Virol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAGLAGLAA
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9; Conser
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                                                                                                                                                                                                                                                                                       75:4854-4870(2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
Herpes_env; 1.
AA; 63743 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=11312357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61852 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.8%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RNA stage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last
Last
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 9;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
BE62EEF35166825D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A297E9DBD094EA74 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence update)
annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              575 AA
                                                                                                                                                                                                                                                                                                                                                       Complete Genome of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 11; Length 555; . 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ₿
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                   Tupaia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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RESULT 38
Q9VZV2
                   AID

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DOC OCCU
RAGEOTGE R.A., Lewis S.E., Richards S., Ashburner M., House, R.A.
Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Button R.C., Rogers Y.-H.C., Blazed R.G., Champe M., Pédiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C.R., Baldwin D.,
RA Bellew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Bellew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Bellew R.M., Basu A., Butter H., Cadleu E., Center A., Chandra I.,
RCherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Burbin K.C., Busam D.A., Butter H., Cadleu E., Center A., Chandra I.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,
Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,
Dunn P.,
RA Gloek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Hellman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeywam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., McLeod M.P., McPherson D.,
RA Kimmel B.E., Kodira C.D., Kraft C., McLeod M.P., McPherson D.,
RA Kimmel B.E., Kodira C.D., Kraft C., McLeod M.P., McPherson D.,
RA McLau O.G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Woy M., Murphy B., Murphy L.M., Murphy D.M., Nelson D.L.,
RA Reihert K., Remington K., Stungeron M., Strong R., Sun E.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Syliskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q. A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q. A.,
RA Globs R.A., Myers E.M., Thomas E.M., Venter E., Wang A.H., Wang X.,
RA Shissen B., Shoodage T., Worley K.C., Wu D., Yang S., Zhu Q., Zheng L.,
RA Globs R.A., Myers E.M., Thomas E.M., Wassenbach J.C.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Zhu Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best
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01-MAY-2000 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D. Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R. George R.A., Lewis S.E., Richards S., Ashburner M., Henderson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ephydroidea; Dro
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pterygota; Neoptera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20196006;
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Q96LC4;
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TIGR; TC0867; -.
PRINTS; PR01608; BACINVASINC.
Hypothetical protein; Complete
SEQUENCE 491 AA; 50762 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                             "Human polyamine oxidase, isoform-2."; submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases EMBL; AY033890; AAK55764.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
          Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases. EMBL; BC000669; AAH00669.1; -
InterPro; IPR000759; Adrindx_reductase.
InterPro; IPR001613; Amino-oxid_fl.
InterPro; IPR002937; Amino_oxidase.
InterPro; IPR002937; Amino_oxidase.
InterPro; IPR00295; NAD_binding.
Pfam; PF01593; Amino_oxidase; 1.
PRINTS; PR00419; ADXRDTASE.
PRINTS; PR00757; AMINEOXDASEF.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence up
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Similar to hypothetical protein.
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InterPro; IPR00205; NAD_binding.
Pfam; PF01593; Amino_oxidase; 1.
SEQUENCE 502 AA; 56156 MW; A6CA
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Mammalia; Eutheria;
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 Hypothetical
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                                                                                                                         TISSUE-KIDNEY;
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Primates;
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Catarrhini;
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InterPro; IPR002937; Amino_oxidase.
InterPro; IPR000205; NAD_binding.
Pfam; PF01593; Amino_oxidase; 1.
PRINTS; PR00419; ADXRDTASE.
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                                                                              "Cloning and characterization of a human inducible by polyamine analogue exposure Cancer Res. 61:5370-5373(2001).
EMBL; AY033889; AAK55763.1;
                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE=21347,206;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
InterPro; IPR002937; Amino oxidase.
InterPro; IPR002055; NAD_binding.
Pfam; PF01593; Amino oxidase: 1.
SEQUENCE 555 AA; 61872 MW; F008
                                                                                                                                                                   Casero R.A. Jr.;
                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                         Wang Y.,
                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                              Polyamine oxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            280 GAGLAGLAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAGLAGLAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity
9; Conser
                                                                                                                                                                                         Devereux W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      555 AA;
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llarity 100.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39
                                                                                                                                                                                                               PubMed=11454677;
                                                                                                                                                                                                                                                                                                                                                              isoform-1.
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Primates;
                                                                                                                                                                                                                                                                                                  Primates;
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                                                                                                                                                                                                                                                                                                                        Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61819 MW;
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                                                                                                                                                                                           Woster P.M.,
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15, Last sequence update)
17, Last annotation update)
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Last annotation updat
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score
                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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F0087D3629013C51 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9;
                                                                                                                                                                                             Stewart T.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         No.
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14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B
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                                                                                                                                 polyamine
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                                                                                                                                                                                                                                                                                                                                                                                     update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 555;
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                                                                                                                                                                                                Hacker
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                                                                                                                                                     oxidase
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RESULT
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Best Local
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EMBL; AY064000; AAL36356.1; -.
InterPro; IPR001613; Amino_oxid_f1.
InterPro; IPR002937; Amino_oxidase.
Pfam; PF00593; Amino_oxidase; 1.
PRINTS; PR00757; AMINEOXDASEF.
SEQUENCE 477 AA; 52258 MW; C33278
                                               SEQUENCE FROM N.A.

STRAIN-D/UW-3/CX;

MEDLINE-99000809; PubMed-978

Stephens R.S., Kalman S., Le

Mitchell W.P., Olinger L., T
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O9SF45;
01-MAY-2000 (TrEMBLrel, 1:
01-MAY-2000 (TrEMBLrel, 1:
01-JUN-2002 (TrEMBLrel, 2:
                                                                                                                                                                                                      01-NOV-1998
01-NOV-1998
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yamanda K., Banh J., Banno F., Chang E., Dale J.M.; Goldsmith A.D. Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G. Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Mirand Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-CV. COLUMBIA;
Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haar
Maiti R., Ronning C.M., Koo H., Fujii C.Y., Utterback T
Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fr
"Arabidopsis thallana chromosome 3 BAC F11F8 genomic see
"Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Putative oxidoreductase.
F11F8_15 OR AT3G09580.
Arabidopsis thaliana (Mouse-ear cress).
"Genome sequence of an obligate Chlamydia trachomatis."; Science 282:754-759(1998).
                                                                                                                                               Chlamydia trachomatis. Bacteria; Chlamydiales;
                                                                                                                                                                                         Hypothetical protein
                                                                                                                                                                                                                                              084582;
                                                                                                                                                                                                                                                          084582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Full Length cDNA of gene At Submitted (NOV-2001) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Theologis A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=3702;
                                        Davis R.W.;
                                                                                                                                    NCBI_TaxID=813;
                                                                                                                                                                                                                                                                                                                                                        280 GAGLAGLAA 288
                                                                                                                                                                                                                                                                                    29
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                                                                                                                                                                                                                                                                                                                             GAGLAGLAA
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3 (TrEMBLrel. 08,
2 (TrEMBLrel. 20,
al protein CT578.
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                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                PubMed=9784136;
lman S., Lammel C.
                                                                                                                                                                                                                                                                                                                                                                                                            1.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21,
                                                                                                                                                Chlamydiaceae;
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                                                      Tatusov
                                                                                                                                                                                                   Created)
Last sequence update)
Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                              Score 9;
Pred. No.
                                                                                                                                                                                                                                                           PRT;
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                            intracellular
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                                                                .J.,
                                                      R.L.,
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o. 12;
                                                                  Fan
                                                                                                                                                Chlamydia
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                                                      Zhao
                                                                  J.,
                                                   0.
                          pathogen of humans
                                                                                                                                                                                                                                                                                                                                                                                                       Length 477;
                                                                  Marathe R.,
                                                     Koonin
                                                                                                                                                                                                                                                                                                                                                                                 Indels
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sequence.";
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                                                                   Aravind
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Cheuk R.,
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RESULT
Q9PJG2
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Best Local S
Matches 9
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                                                                                                                                                                                       Q9PJG2;
Q9PJG2;
01-OCT-2000
01-OCT-2000
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                               Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AY058455; AAL13684.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q95TX7
Q95TX7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata;
Pterygota; Neoptera; Endopterygota; Dipterz
Ephydroidea; Drosophilidae; Drosophila.
                               Read T.D., Brunham R.C., Shen C., Gill S.R., H
White O., Hickey E.K., Peterson J., Uten
Linher K., Weidman J., Khouri H., Craven B., E
Gwinn M., Nelson W., DeBoy R., Kolonay J., McC
Eisen J., Fraser C.M.,
                                                                                      STRAIN=MOPN / NIGG;
MEDLINE=20150255; PubMed=10684935;
                                                                                                                               Chlamydia muridarum.
Bacteria; Chlamydiales;
NCBI_TaxID=83560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-BERKELEY;
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ORK1 OR CG1615
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE001328; AAC68180.1;
"Genome sequences of Chlamydia pneumoniae AR39.";
Nucleic Acids Res. 28:1397-1406
                                                                         Read T.D.,
                                                                                                            SEQUENCE FROM N.A
                                                                                                                                                                     Hypothetical TC0867.
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                          FlyBase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                                               294 AAAAGGAAG
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9; Conserv
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9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                          FBgn0017561; Ork1.
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487 AA; 5
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                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                               302
 28:1397-1406(2000)
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el. 15,
el. 21,
TC0867
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19,
20,
                                                                                                                                            Chlamydiaceae;
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Last annotation update)
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01-NOV-1999
01-JUN-2001
ADP/ATP tran
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Pfam; PF01593; Amino_oxidase; 1.
PRINTS; PR00419; ADXRDTASE.
PROSITE; PR00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
NON_TER 285 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Identification of a cDNA coding for ADP/ATP translocase parasitic nematode Ascaris suum."; Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AR130365; AAD30505.1; -. InterPro; IPR001993; Mitoch_carrier. InterPro; IPR002067; Mit_carrier. Pfam; PP00153; mito_carr; 3. PRINTS; PR00926; MITOCARRIER. UNKNOWN_2. MITOCH_CARRIER; UNKNOWN_2.
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SEQUENCE 307
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[1]
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                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
Babbage A.;
Submitted (FEB-2001) to the
EMBL; AL121675; CAC00598.1;
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                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                             SEQUENCE FROM N.A.
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(TrEMBLrel. 17,
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InterPro; IPR002937; Amino_oxidase.
InterPro; IPR0002937; Amino_oxidase.
InterPro; IPR000205; NAD_binding.
InterPro; IPR000205; NAD_binding.
Pfam; PF01593; Amino_oxidase; 1.
PRINTS; PR00419; ADXRDTASE.
PRINTS; PR00419; ADXRDTASE.
SEQUENCE 308 AA; 33734 MW; FCD4BF469
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Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.
Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
Kutyavin T., Levy R., Li M.-J., McClelland E., Romero P., Gordo
Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordo
Rhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry
Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan J.
Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
Nester E.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2002 (TrEMBLIE1. 21, Crea 01-JUN-2002 (TrEMBLIE1. 21, Last 01-JUN-2002 (TrEMBLIE1. 21, Last 01-JUN-2002 (TrEMBLIE1. 21, Last Secretion protein, HlyD family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Agrobacterium tumefaciens (strain C58 / ATCC Bacteria; Proteobacteria; alpha subdivision;
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                                                                                                                                                                                                                                     "Genome sequence of the plant Agrobacterium tumefaciens C58. Science 294:2323-2328(2001). EMBL; AE009268; AAL44195.1; AL EMBL; AE008344; AAK90008.1; -
                                                                                                                                                                                                                                                                                                                                                            Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin
Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B
Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
Cielo C., Slater S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rhizobiaceae; Rhizobium. NCBI_TaxID=176299;
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  64
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12;
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                                                                                                                          Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., Harris D.E., Quail M.A., Kieser H., Clins M., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S., Taylor K., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTHIBLE J., HOMETOVA D., SEVCÍKOVA B., NOVAKOVA R., Blaskovic D.; "Large subunit of glutamate synthase of Streptomyces coelicolor A3(2).";
                                 Pfam; PF01988; SEQUENCE 243
                                                                               "Complete genome sequence coelicolor A3(2).";
Nature 417:141-147(2002).
                                                                                                                                                                                                                       STRAIN=A3(2) / M145;
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                                                                                                                                                                                                                                                        Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic the 8 mb Streptomyces coelicolor A3(2) chromosome Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                     MEDLINE=97000351;
                                                                                                                                                                                                                                                                                                                                    STRAIN-A3(2);
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James K.D., P
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Seeger K.J.,
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Bacteria; Firmicutes; Actinobacteria;
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01-MAY-2000
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                                                                      EMBL;
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Kieser H.M., Denapaite
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                                              DUF125;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         coelicolor A3(2).";
Nature 417:141-147(2002).
EMBL; AL390188; CAB99157.1;
                             reductoisomerase gene harboring locus isoprenoid blosynthesis.; rEBS Lett. 481:221-226(2000). EMBL: AJ250721; CAB65434.1; -.
                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
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Actinomycetales; Streptomycineae; Streptomycetaceae;
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01-OCT-2000
                                                                                                                                                                 Bacteria; Cyanobacteria;
                                                                                                                                                                             Synechococcus leopoliensis
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                                                                                           Miller B., Heuser T., Zimmer
                                                                                                      MEDLINE-20465103;
                                                                                                                    STRAIN-SAUG 1402-1;
                                                                                                                               SEQUENCE FROM N.A
                                                                                                                                                    NCBI_TaxID=32047;
                                                                                                                                                                                                    Zeta carotene
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MEDLINE-94140364; PubMed=8307574;
Lin D., Chang Y.J., Strauss J.F., Miller W.L.;
"The human peripheral benzodiazepine receptor gene: cloning characterization of alternative splicing in normal tissues patient with congenital lipoid adrenal hyperplasia.";
Genomics 18:643-550(1993).
EMBL; L21954; AAA18228.1; -.
EMBL; L21953; AAA18228.1; JOINED.
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Q96TF6;
01-DEC-2001
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 20, Last annotation update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DJ526I14.1 (benzodiazapine receptor (peripheral) (PBR,
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01-DEC-2001
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01-MAY-2000
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Q95440
ID Q9544
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Bao W.G., Huo K.K., Li Y.Y., Fukuha
Prottein disulfide isomerase genes
Yeast 16:329-341(2000);
EMBL; AJ243960; CAB51777.1; -.
NON_TER
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01-DEC-2001
01-JUN-2002
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
NCBI_TaxID=28985;
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Q9S440;
Q1-MAY-2000
Q1-MAY-2000
Q1-JUN-2001
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                                                                                                                                                                                                                                                                                                                Wang Y., Devereux W., Stewart T.M., Hacker A., "Human polyamine oxidase, isoform-3."; submitted (MAY-2001) to the EMBL/GenBank/DDBJ EMBL; AY033891; AAK55765.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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Mammalia; Eutheria;
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InterPro; IPR000205; MaD_bindi
Pfam; PF01593; Amino_oxidase;
SEQUENCE 190 AA; 20616 MW;
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                            Streptomyces coelicolor A3(2).
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=100226;
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 SEQUENCE FROM STRAIN-M145;
                                                                                  H3U (Fragment).
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Primates;
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NAD_binding.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C3D8EB079CE4661A CRC64;
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annotation
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Kluyveromyces lactis.";
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AC Q9LY0
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Q94FQ7;
01-DEC-2001
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01-DEC-2001 (TrEMBLrel. 20, Last sequence updo
01-MAR-2002 (TrEMBLrel. 20, Last annotation updo
01-MAR-2002 (TrEMBLrel. 20, Last annotation updo
01-MAR-2005 (TrEMBLrel. 20, Last annotation updo
01-DEC-2001 (TrEMBLrel. 20, Last annotation updo
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"Gene families from the Arabidopsis thaliana

Science 292:2482-2485(2001).

EMBL; AF362475; AAK83832.1; -.

InterPro; IPR000136; Oleosin.

Pfam; PF01277; Oleosin; 1

SEQUENCE 147 AA; 14878 MW; C3FEE84BC4F5C0
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MEDLINE-21324873; PubMed-11431566;
Mayfield J.A., Fieblig A., Johnstone S.E., Pre
"Gene familles from the Arabidopsis thaliana
             T2I1_270
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EMBL; AF362476; AAK83838.1; -.
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(TIEMBLIEL 19, Last sequence update)
(TIEMBLIEL 20, Last annotation update)
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ana pollen
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Q94FR2;
Q94FR2;
01-DEC-2001
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01-DEC-2001 (TrEMBLrel. 19, Last sequence updated)
01-MAR-2002 (TrEMBLrel. 20, Last annotation updated)
Glycine-rich protein GRP20.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryosperiatory, Wagnoliophyta; eudicotyledons;
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EMBL; AF362477; AAK83839.1; -.
InterPro; IPR000136; Oleosin.
Pfam; PF01277; Oleosin; 1.
SEQUENCE 153 AA; 15458 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Bevan M., Murphy G., Ridley
Rudd S., Lemcke K., Mayer K.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                               Science 292:2482-2485(2001).
EMBL; AF362474; AAK83826.1;
                                                                                                                                                                                                                                                                                               MEDLINE-21324873; PubMed-11431566; Mayfield J.A., Fiebig A., Johnstone "Gene families from the Arabidopsis"
                                                                                                                                                                                                                                                                                                                                                                               eurosids II; Brassicales; Brassicaceae; NCBI_TaxID=3702;
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    PF01277; Oleosin; 1.
    NCE    153 AA; 15486 MW;
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9; Conser
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ilarity 100.0%;
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Pred. No
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thaliana pollen
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thaliana pollen
169
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                                                                                                                                                                DB 10;
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edons; core eudicots; Rosidae;
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Matches 9; Conserv
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SEQUENCE FROM N.A.

Vierny C., Folichon M., Silar P.;

Vierny C., Folichon M., Silar P.;

"Ribosomal proteins of Podospora anserina.";

"Ribosomal proteins of Podospora anserina.";

"Ribosomal proteins of Podospora anserina.";

RemBL, AF331715; AAK11263.1;

REMBL; AF331715; AAK11263.1;

RICEPTO; IPRO01813; 60s_ribosomal.

PRINTO; IPRO01859; Ribosomal.P2.

RICEPTO; IPRO01859; Ribosomal. 1.

DR Pfam; PF00428; 60s_ribosomal; 1.

DR PFAM; PF00428; 60s_ribosomal; 2.

PRINTO; PR00456; RIBOSOMALP2.

DR PRINTO; PR00456; RIBOSOMALP2.
                                                                                                                                     Query Match
Best Local S
Matches 9
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; mitosporic Hypocreales; Fusarium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
60S acidic ribosomal protein P2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases EMBL; AY077706; AAL79930.1; Ribosomal protein. SEQUENCE 109 AA; 11036 MW. DORPADDATATE ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8TFM9;
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NCBI_TaxID=5516;
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||||||||||
67 AAAAGGAAG 75
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Hoff M., Krail M., Vieths S., Haustein D.;

"Igg-binding acidic ribosomal protein P2 is a potential allergen

Fusarium culmorum.";

The Pure / Contant / DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9C3Z5 PRELIMINARY; PRF; III AA.
Q9C3Z5;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
Q1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 18, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ribosomal protein P2.

Podospora anserina.

Podosyota; Fungi; Ascomycota; Pezizomycotina;

Sordariales; Lasiosphaeriaceae; Podospora.

NCBI_TaxID=5145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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                                                                        293 GAAAAGGAA 301
72
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9; Conservative
                                                                                                                                                Similarity 9; Conser
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ilarity 100.0%;
Conservative
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                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84
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100.0%; Pr
'''a 0;
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Pred. No.
                                                                                                                                                    score 9; DB 3; Pred. No. 3.6
0; Mismatches
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Q8V7C9
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           RESULT
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Query Match
Best Local S
Matches 9
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Arch. Virol. 147:21-41(2002).
EMBL; ABB064624; BAB79391.1;
Interpro; IPR004118; TT_ORF2.
Pfam; PF02957; TT_ORF2: 1.
                                                        Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08V7C9;
08V7C9;
01-MAR-2002
01-MAR-2002
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORF2.
TT virus.
Viruses; ssDNA viruses;
                                                                                                        MEDLINE=21844401; PubMed=11855633; MEDLINE=21844401; PubMed=11855633; MEDLINE=1844401; PubMed=11855633;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Okamoto H.;
                                                                                                                                                                                                                                                                                                                     01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
peripheral-type benzodiazepine receptor (Fragment).
                                                                                                                                                                                                                                                                   PBR.
Homo sapiens (Human).
Homo sapiens (Human).
Horida; Metazoa; Chordata;
Horida; Primates;
                                                                                                                                                                                               SEQUENCE FROM N.A.
TISSUE=BREAST;
Hardwick M.J., Papadopoulos V.;
"Peripheral-type Benzodiazepine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       298 GGAAGAAAA 306
                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                               SEQUENCE
                      302 GAAAATTVA 310
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GAAAATTVA
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9; Conserv
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9; Conserv
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nilarity 100.0%;
Conservative 0
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                                              1.8%;
nilarity 100.0%;
Conservative 0
                                                                                                143 AA;
                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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AA; 13219 MW;
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  99
                                                                                                    16107 MW;
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; Pred. No
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                                                               Score 9; D
                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                     DEAF74A8415C65A9 CRC64;
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                                                                                                                                                                                                      Receptor
                                                      Mismatches
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                                                                  DB 4;
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(on update)
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                                                                                                                                                                                 databases
                                                                              Length 143;
                                                                                                                                                                                                         in Human Breast
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                                                                                                                                                                                                                                                                                                                                           O9FU65 PRELIMINANI,
O9FU65;
O1-MAR-2001 (TrEMBLrel. 16, Created)
O1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
On-weighting the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of
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O1-JAN-1998
O1-JAN-1998
                                                                                                                                                                                 Oryza sativa (Rice).

Bukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.

NCBI_TaxID=4530;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97445059; PubMed=9300048;
Leigh Brown A.J., Lobidel D., Wade C.M., Rebus S., Phillips
Brettle R.P., France A.J., Leen C.S., McMenamin J., McMillan
Maw R.D., Mulcahy F., Robertson J.R., Sankar K.N., Scott G.,
Peutherer J.F.;
"The molecular epidemiology of human immunodeficiency virus
six cities in Britain and Ireland.";
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          clone: P0013F10.";
                              STRAIN=CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yama
"Oryza sativa nipponbare(GA3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00540; Gag_p17; 1.
AIDS; Core protein; Polypr
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EMBL; AF014293; AAC58374.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Viruses; Retroid viruses; NCBI_TaxID=11676;
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                                                                                                                                     SEQUENCE FROM N.A.
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ilarity 100.0%; Conservative 0;
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larity 100.0%; Pred. No.
Conservative 0; Mismatc
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                                                                  Yamamoto
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                                 DNA,
                                                                                                                                                                                                                                                              Embryophyta; Tracheophyta; a; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 15; Length 137; 0.49;
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0.46;
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                                    chromosome
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Best Local
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01-JUN-2002 (TrEMBLrel. 2
01-JUN-2002 (TrEMBLrel. 2
01-JUN-2002 (TrEMBLrel. 2
P0470A12.43 protein.
P0470A12.43.
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Q8S076;
01-JUN-2002
       Abramczyk D., Tchorzewski M., Grankowski N.; "Cloning, expression and purification of the a from Candida albicans."; submitted (NOV-2000) to the EMBL/GenBank/DDBJ EMBL, AF317659; AAG33240.1; ". InterPro; IPR001813; 60s_ribosomal. Pfam; PF00428; 60s_ribosomal; 1. Ribosomal protein.
                                                                                                                                                                                              01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-JUN-2001 (TrEMBLrel. 17, 60S acidic ribosomal proteir
                                                                                                                                                                                                                                            Q9HFQ7
Q9HFQ7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JUN-2000) to the EMBL; AP002523; BAB17063.1; Interpro; IPR004249; NPH3. Pfam; PF03000; NPH3; 1. SEQUENCE 487 AA; 50508 MW
                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases EMBL; AP003436; BAB90315.1; -. SEQUENCE 103 AA; 10426 MW; 4A1EA91B1477B35B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yaman
"Oryza sativa nipponbare(GA3)
clone:P0470A12.";
                                                                                                    SEQUENCE FROM N.A. STRAIN=CCM 8215;
                                                                                                                                                   Saccharomycetales;
                                                                                                                                                            Candida albicans (Yeast).
Eukaryota; Fungi; Ascomyo
                                                                                                                                      NCBI_TaxID=5476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=39947;
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                                                                                                                                                                                                                                                                                                                  17 AAAAGGAAG
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10; Conser
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9; Conser
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protein.
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ilarity 100.0%;
Conservative
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llarity 100.0%
Conservative
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                                                                                                                                                 Ascomycota; mitosporic
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MW;
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n type P1-A.
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Pred. No
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Pred.
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) genomic
                                                                                                                                                  Saccharomycotina; Saccharomycetes; Saccharomycetales; Candida.
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BB03BB1B0CE9547E CRC64;
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A Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
A Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
A Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
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A Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc Ephydroidea; Drosophilidae; Drosophila.
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RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Meson D.R., Nelson K., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Melson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Sunders R.D.C., Scheeler F., Shen H.,
RA Spier B.C., Siden-Kiamos I., Simpson M., Strong R., Smith T.,
RA Sylrskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Rublin G.M., Venter J.C.,
RTHe genome sequence of Drosophila melanogaster.";
RMBL, Accolo3442; AAF46312.2; -.
REMBL, Accolo3442; AAF46312.2; -.
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HSSP; Q92831; 1B91.
FlyBase; FBgn0004656; fs(1)h.
InterPro; IPR001487; Bromodomain.
InterPro; IPR002193; Kininogen.
InterPro; IPR002173; PfKB.
Pfam; PF00439; bromodomain; 2.
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PRINTS; PR00334; KININOGEN.
SMART; SM00297; BROMO; 2.
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PROSITE; PS50014; BROMODOMAIN_2; 2.
PROSITE; PS500583; PFKB_KINASES_1; U
PROSITE; PS00583; PFKB_KINASES_1; U
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Viruses; dsDNA viruses, no F
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Q9Z797;
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01-MAY-1999
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KRaiman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
"Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
Nat. Genet. 21:385-389(1999).
Nat. Genet. 21:385-389(1999).
TRIBD. AE001662; AAD18947.1;
InterPro. IPR000508; SigpProSE.
                                                                                                                                                                                                                                                                                           CT578 hypothetical protein CPN0809.
                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                       Chlamydia pneumoniae (Chlamydophila Bacteria; Chlamydiales; Chlamydiacea RCBI_TaxID=83558;
                                                                                                                      InterPro, IPR000508;
PROSITE; PS00501; SP
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                       4
            MSISSSSGPDNQKNIMSQVLTSTPQGVPQQDKLSGNETKQIQQTRQGKNTEMESDATIAG
MSISSSGPDNQKNIMSQVLTSTPQGVPQQDKLSGNETKQIQQTRQGKNTEMESDATIAG
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493 AA;
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SPASE_I_1; UNKNOWN_1.
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Q9HYA3
Q9VWJ2
Q9AAY7
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Q8U913
Q8U918
Q918H6
Q97UN3
Q9FV45
Q92KE8
Q98CQ8
Q9FV10
Q9FXL6
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O65563 bovine herp
O91642 pseudomonas
O93774 oryza sativ
O8vx08 gentiana
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013510 rhodotorula
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Q95u47 drosophila
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Read T.D., Brunham R.C., Shen C., Gill S.R., Heir Mhite O., Hickey E.K., Peterson J., Utterback T. Linher K., Weidman J., Khouri H., Craven B., Bown Gwinn M., Nelson W., DeBoy R., Kolonay J., McCla. Eisen J., Fraser C.M.;
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         Q94FQ7
Q94FQ2
Q9LY07
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Q9z797 ohlamydia p
Q9j566 chlamydia p
Q9j566 chlamydia p
Q9s313 drosophila
Q9s279 molluscum c
Q9s279 molluscum c
Q9f165 oryza sativ
Q8s076 oryza sativ
Q9hf97 candida alb
Q8tfm9 fusaxium cu
Q9c3z5 podospora a
Q8v7c9 tt virus. o
Q76068 homo saplen
Q94fq7 arabidopsis
Q94fq2 arabidopsis
Q94fq2 arabidopsis
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       16 OBUAJI
10 OSSF45
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018333
                    Q8UD60
Q9F2R7
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Q9BIT4
Q9H8P1
Q9H8P1
G9XAI2
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Q9M0L8
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ogszy4 streptomyce
ogyrct2 synechococc
ogymn22 ascaris suu
ogspy2 homo sapien
ogsu43 arabidopsis
ogs445 arabidopsis
ogs445 arabidopsis
ogs4582 chlamydia t
ogsf147 drosophila
ogspj92 chlamydia m
ogs614 homo sapien
ogsm0 homo sapien
ogsm0 homo sapien
ogsw18 homo sapien
ogsy88 homo sapien
ogsy88 homo sapien
ogs614 homo sapien
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ogs617 homo sapien
ogs618 musculu
ogs1160 arabidopsis
ogw010 oryza sativ
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ogs6285 mycobacteri
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ggu347 caenorhabdi
ggu348 caenorhabdi
ggu387 caenorhabdi
gro76786 antheraea y
g96444 antheraea y
g96444 antheraea y
g9upd8 homo sapien
g92057 gallus gall
g4112 pneumocysti
g8r412 mus musculu
g8u5y agrobacteri
g4018 candida alb
g9ns64 homo sapien
g91372 mus musculu
g964717 rhodotorula
a43180 homo sapien
g91372 mus musculu
g96474 pseudomonas
g9rrg3 deinococcus
g9rg3 deino

Q8ud60 agrobacteri Q9f2r7 streptomyce Q8rnx8 propionibac Q9bit4 nephila sen Q9h8p1 homo sapien

Q9xai2 streptomyce 050464 mycobacteri Q9ki88 bacillus ce

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SETTETT TO THE TETTETT N54_CAEEL
ID YN54_C.
AC P3458A
AC P3458A
D1 01-FEB
D1 15-JUN
DE Hypoth
GN ZC21.4
OS Caenor
OC Eukary
OC Rhabdi
OX NCBL_T
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Matches 8
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-i- DOMAIN: Highly repetitive protein characterized polyalanine and glycine-rich repeating units.
-i- SIMILARITY: BELONGS TO THE SILK FIBROIN FAMILY.
                                                                           01-FEB-1994 (
01-FEB-1994 (
15-JUN-2002 (
Hypothetical
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 Eukaryota; Metazoa; Rhabditidae; Pelode NCBI_TaxID=6239;
                                             Caenorhabditis elegans.
                                                                                                                                                                                                                                      624
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U03848; AAB60212.1;
                                                                                                                                                                                                                                      GAAAAGGA 631
                                                                                                                                                                                                                                                                                                  Similarity
8; Conser
                                                                                                                                                                                                                                                                                                                                                                 747 AA;
                                                                           (Rel. 28, Created)
(Rel. 28, Last sequence update)
(Rel. 41, Last annotation update)
l protein ZC21.4 in chromosome III
                                                                                                                                                                                                                                                                                                                                                                                                             A36068.
                                                                                                                                                                                                                                                                                                  Conservative
                   Peloderinae;
                                                                                                                                                           STANDARD;
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                                  Nematoda;
                                                                                                                                                                                                                                                                                                                   100.0%;
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                 oda; Chromadorea; Rhabditida; Rhabditoidea; Caenorhabditis.
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Pred. No.
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S -> T (IN REF. 1).
NPGL/SGCDVLIQALLEVYSALIQILGSS/SIGOVNYGSAGQA
TQIVGQSVYQAL -> ILVFLDVMSSFKLFSRLFLLLSRS
(IN REF. 1).
, 850E44B0D649E012 CRC64;
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b. 27;
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SEQUENCE FROM N.A.
STRAIN-Bristol N2;
MEDLINE-94150718; P
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A
Bonfield J., Burton J., Connell M., Fraser A.,
Fraser A.,
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Fraser A.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N., Johnston L., Jones M., Callaghan M.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen J.
Sims M., Smaldon N., Smith M., Sonnhammer E., Staden R.,
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
Rocklamp P.
                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.";
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                                                                                                                                                                           WormPep; ZC21.4; CE00534.
InterPro; IPR000198; RhoGAI
Pfam; PF00620; RhoGAP; 1.
SMART; SM00324; RhoGAP; 1.
                                                                                                                                         Hypothetical protein. SEQUENCE 747 AA; 8
                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: CONTAINS 1 RHO-GAP DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 368:32-38(1994)
495 GAAGAAAA
                                  299 GAAGAAA
                                                                                                                                                                                                                                                   Q07960;
                                                                                                                                                                                                                                                                    L16685; AAA28171.1; ALT_INIT.
                                                                  Similarity
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Pred. No
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RESULT 43
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P51802;
01-OCT-1996
01-OCT-1996
15-JUN-2002
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PROSITE; PS00518; ZF_RING_1; FALSE_NEG PROSITE; PS50089; ZF_RING_2; 1.
           or send a
                                                                                                                                                                                                                                                              Jascending limb of Henle's loop and collecting ducts of rat kidne J. Biol. Chem. 269:11677-17683(1994)
-i- FUNCTION: VOLTAGE-GATED CHLORIDE CHANNEL. CHLORIDE CHANNELS SEVERAL FUNCTIONS INCLUDING THE REGULATION OF CELL VOLUME;
                                                                                                                                                                                                                                                                                                                                                                                                                                            "Two
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Pfam; PF00097; zf-C3HC4; 1.
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Adachi S., Uchida
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kieferle
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F
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                                                                                                                                                      SUBCELLULAR LOCATION: Integral membrane protein.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; CLC-K2L (SHOWN HERE) AND
K2S; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN THE KIDNEY.
EXPRESSED IN ALL SEGMENTS OF THE NEPHRON EXAMINED, INCLUDIN
                                                             s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restr
                                                                                                               S2 SEGMENT AND THE GLOMERULUS.
SIMILARITY: BELONGS TO THE CHLORIDE CHANNEL FAMILY.
SIMILARITY: CONTAINS 2 CBS DOMAINS.
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                                                                                                                                                                                                                                                                                                                                                                                                                             erle S., Fong P., Bens M., Vandewalle highly homologous members of the ClC rat and human kidney.";
                                                                                                                                                                                                                                                                                                      isoforms of a chloride channel predominantly expressed in nding limb of Henle's loop and collecting ducts of rat kid
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HGNC:12968; ZNF179.
            an
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8; Conserv
         non-profit institutions as long as its content is in no way and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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S., Hata M., Hirose M.,
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68354 MW;
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Pred. No.
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                                                             There are no restrictions
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chloride channel family
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SPD1_NEPCL
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Best Local
"Sequence conservation in the C-terminal region of spider silk proteins (Spidroin) from Nephila clavipes (Tetragnathidae) and Araneus bicentenarius (Araneidae).";
J. Biol. Chem. 269:661-663(1994).
-!- FUNCTION: Spiders major ampullate silk possesses unique characteristics of strength and elasticity. Fibroin consists of pseudocristalline regions of antiparallel beta-sheet interspersed with elastic amorphous segments.
-!- SUBUNIT: MAJOR SUBUNIT, WITH SPIDROIN 2, OF THE DRAGLINE SILK.
                                                                                                                                                                                                                                                                                                                                                                                                                                          VARSPLIC
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                                                                                                                                                                                                                                         01-FEB-1991 (Rel. 17, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Spidroin 1 (Dragline silk fibroin 1) (Fragment).
                                                                                                                                                                                                                                                                                    SPD1_NEPCL P19837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000644; CBS_domain.
InterPro; IPR001807; C1-Channel_volt.
Pfam; PF00571; CBS; 2.
Pfam; PF00654; voltage_CLC; 1.
                                                                                                                                      "Structure of a protein superfiber: spider dragline silk."; Proc. Natl. Acad. Sci. U.S.A. 87:7120-7124(1990).
                                                                                                                                                                             SEQUENCE FROM N.A.,
                                                                                                                                                                                                           Araneomorphae; Entelegynae; Araneoidea; Tetragnathidae;
                                                                                                                                                                                                                      Nephila clavipes (Orb spider).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida;
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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SMART; SM00116; CBS; 1.
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EMBL; D26111; BAA05106.1;
EMBL; D26111; BAA05107.1;
                                                                                          Beckwitt R., Arcidiacono S.;
                                                                                                      MEDLINE-94165058;
                                                                                                                  SEQUENCE OF 653-747 FROM N.A.
                                                                                                                                                           Xu M., Lewis R.V.;
                                                                                                                                                                    MEDLINE=90384959;
                                                                                                                                                                                                 NCBI_TaxID=6915;
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                                                                                                         PubMed-8120021;
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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Pred. No. 26;
Mismatches
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                   070418;

16-0CT-2001 (Rel. 40, Created)

16-0CT-2001 (Rel. 40, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)

Zinc finger protein 179 (Brain finger protein)

ZNF179 OR BFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 METAL
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Pfam; PF00115; COX1; 1.
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HSSP; P18401; 1FFT.
                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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   SEQUENCE FROM N.A.
MEDLINE=98042506; PubMed=9367872;
                                                                                                                                                                                                                  Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             280 GAGLAGLA 287
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CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome c + 2 H(2)O.

PATHWAY: Respiratory chain; terminal step.

PATHWAY: Respiratory chain; terminal step.

SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane. Contains 12 potential transmembrane domains.

SIBLEARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.

CAUTION: SOME POSITIONS ARE MODIFIED BY RNA EDITING.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biol. Chem. 268:25483-25486(1993). FUNCTION: Cytochrome c oxidase is the component of the
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8; Conserv
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87
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Conservative
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IRON (HEME A) (PROBABLE).
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IRON (HEME A3) (PROBABLE).
IRON (HEME A) (PROBABLE).
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                                                                                                                                                      Sciurognathi;
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"A nowel RING finger protein, BFP, predominantly expressions of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O9ULX5; 060633;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Zinc finger protein 179 (Brain finger protein).
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Pfam; PF00097; zf-C3HC4; 1.
SMART; SM00184; RING; 1.
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                                                                                                                                                                                                                                                       finger protein (bfp), a member of the RING ringe Genomics 33:325-327(1996).
-- TISSUE SPECIFICITY: Predominantly expressed.
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 33-127 FROM N.A. MEDLINE=96301415; PubMed=866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seki N., Hattori A.,
"Human BFP/ZNF179.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         583
                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                           the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                   Matsuda Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted
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                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                   01415; PubMed=8660987; Inoue S., Seki N., Ho
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Q8Y5R9;
15-JUN-2002
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Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Charbit A., Chetouani F., Couve E., de Darwar A., Dehoux P.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
Entian K.-D., Fsihl H., Garcia-del Portillo F., Garrido P.,
Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
"Comparative genomics of Listeria species.";
Science 294:849-852(2001).
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                                                                           Interpro; IPR002034; AIPM/Hcit_synth.
Interpro; IPR002034; HMGL-1ike.
Pfam; PP00682; HMGL-1ike; 1.
TIGRFAMS; TIGR00973; leuA_bact; 1.
PROSITE; P$00815; AIPM_HOMOCIT_SYNTH_1; 1.
PROSITE; P$00816; AIPM_HOMOCIT_SYNTH_2; 1.
Leucine biosynthesis; Lyase; Complete prot
SEQUENCE 512 AA; 56096 MW; 5AAB1D633D3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      synthase) (Alpha-IPM synthetase).
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                                                                                                                                                                                                                                        modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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MEDLINE=21537279; PubMed=11679669;
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Bacteria; Firmicutes;
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2-isopropylmalate synthase (EC 4.1.3.12) (Alpha-isopropylmalate
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15-JUN-2002 (Rel. 41, Last annotation
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                                    Local
                                                                                                                                                                                                                           send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                               FUNCTION: Catalyzes the condensation of the acetyl group of acetyl-CoA with 3-methyl-2-oxobutanoate (2-oxoisovalerate) to form 3-carboxy 3-hydroxy 4-methylpentanoate (2-isopropylmalate).

CATALYTIC ACTIVITY: 3-carboxy-3-hydroxy-4-methylpentanoate + CoA = acetyl-CoA + 3-methyl-2-oxobutanoate + H(2)O.

PATHWAY: Leucine biosynthesis; first step.

SUBUNIT: Homotetramer (By similarity).

SIMILARITY: BELONGS TO THE ALPHA-IPM SYNTHETASE / HOMOCITRATE
                                                                                                                                                                                                                                                                                                                                  SYNTHASE FAMILY. LEUA 1 SUBFAMILY.
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                       1.6%; Solitarity 100.0%; If Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Nature 387:394-401(1997).
-i- FUNCTION: PROBABLY PART OF A BINDING-PROTEIN-DEPENDENT TRANSPORT
-yrstem y4TOPQRS FOR A PEPTIDE.
-i- SUBCELLULAR LOCATION: Periplasmic (Potential).
-i- SIMILARITY: BELONGS TO THE BACTERIAL EXTRACELLULAR SOLUTE-BINDING
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                                                                     Physarum polycephalum
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MEDLINE=97305956; PubMed=9163424;
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Myxogastria; Myxogastromycetidae; Physarida;
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Pfam; PF01593; Amino_oxidase; 1.

Carotenoid biographhesis; Oxidoreductase; FAD; Flavoprotein;
Carotenoid biographhesis; Oxidoreductase; FAD; Flavoprotein;
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NP_BIND 7 23 FAD (ADP PART) (POTENTIAL)

VARIANT 195 195 R -> C (CONFERS RESISTANCE)
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Zeta-carotene desaturase (EC 1.14.99.30) (Carotene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cyanobacterium Anabaena sp. strain PCC 7120.";

DNA Res. 8:205-213(2001).

-i- FUNCTION: Catalyzes the conversion of zeta-carotene to lycopene via the intermediary of neurosporene. It carries out two consecutive desaturations (introduction of double bonds) at positions C-7 and C-7' (By similarity).

-i- CATALYTIC ACTIVITY: Zeta-carotene + AH(2) + O(2) = neurosporene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yasuda M., Tabata S.;
"Complete genomic sequence of the filamentous nitrogen-fixing"Complete genomic sequence of the filamentous nitrogen-fixing
                                                                                                                                                             use by non-profit institutions as long as its content modified and this statement is not removed. Usage by are entities requires a license agreement (See http://www.isb-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21595285; PubMed=11759840;
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                      InterPro;
InterPro;
                                             EMBL; Y15115; CAB56041.1; -
EMBL; AP003589; BAB74081.1;
InterPro; IPR002937; Amino-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36
                                                                                                                                              or send
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                                                                                                                                                                                                                                                                                                                                         PATHWAY: Carotenoid biosynthesis.
SIMILARITY: BELONGS TO THE ZETA CAROTENE DESATURASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          s20939;
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CATALYTIC AC
                                                                                                                                                                                                                                                                                                                                                                COFACTOR: NAD, NADP, PATHWAY: Carotenoid
                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the E
     PF01593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ipr002937; Amino_oxidase.
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                              IPR000205;
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                                                                                                                                                equires a license agreement (S email to license@isb-sib.ch).
                                                                                                                                                                                                                                         Bioinformatics Institute.
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PROSITE;

Leucine biosynthesis; SEQUENCE 512 AA; 5

PS00815; AIPM\_HOMOCIT\_SYNTH\_1; 1.
PS00816; AIPM\_HOMOCIT\_SYNTH\_2; 1
PS00816; AIPM\_HOMOCIT\_SYNTH\_2; 1
PS00816; AIPM\_HOMOCIT\_SYNTH\_2; 1
PS00815; AIPM\_HOMOCIT\_SYNTH\_1; 1
PS00816; AIPM\_HOMOCIT\_SYNTH\_1; 1

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Best Local S
Matches
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RA Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominquez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Domann E., Dominquez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Gautier L., Goebel W., Gancia-del Portillo F., Garrido P.,
RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
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RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Ng Ling Raitournam A., Mata Vicente J., Ng E., Ng Ling Raitournam A., Mata Vicente J., Ng E., Ng Ling Raitournam A., Mata Vicente J., Ng E., Ng Ling Raitournam A., Mata Vicente J., Ng E., Ng Ling Raitournam A., Mata Vicente J., Ng E., Ng Ling Raitournam A., Mata Vicente J., Ng E., Ng Ling Raitournam A., Mata Vicente J., Ng E., Ng Ling Raitournam A., Mata Vicente J., Ng E., Ng Ling Raitournam A., Mata Vicente J., Ng E., Ng Ling Raitournam A., Mata Vicente J., Ng E., Ng Ling Raitournam A., Mata Vicente J., Ng E., Ng Ling Raitournam A., Mata Vicente J., Ng E., Ng Ling Raitournam A., Mata Vicente J., Ng E., Ng Ling Raitournam A., Mata Vicente J., Ng E., Ng Lin
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CONFLICT 92
SEQUENCE 479 AA;
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2-isopropylmalate synthase (EC 4.1.3.12) (Alpha-isopropylmalate synthase) (Alpha-IPM synthetase).
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STRAIN=CLIP 11262 / Serovar 6a;
MEDLINE=21537279; PubMed=11679669;
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Bacteria; Firmicutes;
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15-JUN-2002 (Rel.
15-JUN-2002 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=1642;
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                                                                                                                                                                                                   entities requires a license agreement (Son send an email to license@isb-sib.ch).
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                                                                           InterPro; IPR002034; AIPM/Hcit_synth.
InterPro; IPR000891; HMGL-like.
Pfam; PF00682; HMGL-like; 1.
TIGRPAMS; TIGR00973; leuA_bact; 1.
                                                                                                                                                                  EMBL; AL596171; CAC97324.1; -.
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                                                                                                                                                   ListiList; LIN02094;
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SUBUNIT: Homotetramer (By Similarity)
SIMILARITY: BELONGS TO THE ALPHA-IPM
SYNTHASE FAMILY. LEUA 1 SUBFAMILY.
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8; Conser
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                                                                                                                                                                                                                                                                 Bioinformatics Institute. The profit institutions as long
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19;
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RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Deloukas P., Matthews L.H., Ashurst J., Bard L.M., Beare D.M.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Balley J.D., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
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RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Clington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Clington A.G., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., McLay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Whitehead S.L., Whittaker P., Willey D.L., Walliams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Roders M.
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Created)
Molybdenum cofactor synthesis protein 3 (Molybdopterin synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stallmeyer B., Coyne K.E., W
Rajagopalan K.V., Mendel R.R
The cDNA sequence of MOCS3,
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Eukaryota; Metazoa;
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                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                the
                                                                                                                                                                                                                                                                                                                                                                                       Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases -i- FUNCTION: Activates MPT synthase by the ATP dependan
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                                                                                                                                                                                                            European
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AL034553; CAB53750.1;
BC015939; AAH15939.1;
                                      HGNC:15765; MOCS3.
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                                                                                                                                                                       pean Bioinformatics Institute. The non-profit institutions as long and this statement is not removed.
                                                                                                                                                                                                                                    the Swiss Institute of Bioinformatics
IPR000205;
IPR001763;
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Mendel R.R.;
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                  NAD_binding
    Rhodanese-like
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P29273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yanada M., Yasuda M., Tabata S.; Yanada M., Yasuda M., Tabata S.; Yanada M., Sasa S.; Yanada M., Sasa S.; Sequence analysis of the genome of the unicellular cyanobacterium "Sequence analysis of the genome of the unicellular cyanobacterium entire genome and assignment of potential protein-coding regions.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00450; RHOD; 1.
Ligase; Molybdenum cofactor biosynthesis.
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01-FEE-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Phytoene dehydrogenase (EC 1.14.99.-) (Phytoene desaturase).
PDS OR CRTD OR SLR1254.
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Pfam; PF00581;
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"Nucleotide sequence of the phytoene desaturase gene from
Synechocystis sp. PCC 6803 and characterization of a new mutation
which confers resistance to the herbicide norflurazon.";
Plant Mol. Biol. 18:981-983(1992).
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                                                                                                                                                                                  the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed
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                                                                                                                or send an email to license@isb-sib.ch).
                                      EMBL; X62574;
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SIMILARITY: BELONGS TO THE PHYTOENE DEHYDROGENASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PATHWAY: Carotenoid biosynthesis.
SUBCELLULAR LOCATION: Membrane-associated (Probable)
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           CAA44452.1;
BAA17847.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rhodanese;
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Pred. No
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Mismatches
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18;
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HYPB_ALCEU
RESULT 33
TRMU_MYCTU STANDARD;
ID TRMU_MYCTU STANDARD;
AC 053271;
AC 053271;
DT 30-MAY-2000 (Rel. 39, Created)
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Best Local (
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01-JUL-1993 (Rel. 26, C
01-NOV-1995 (Rel. 32, I
16-OCT-2001 (Rel. 40, I
Hydrogenase nickel inco
                                                                                                                                                 Matches
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-H16 / DSM 428 / ATCC 17699;
Eitinger T.;
Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: COULD BE INVOLVED IN NICKEL BINDING AND AC-
-i- SIMILARITY: BELONGS TO THE HYPB/HUPM FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-H16 / DSM 428 / ATCC 17699;
STRAIN-H16 / DSM 428 / ATCC 17699;
MEDLINE-93356597; PubMed-8352644;
Dernedde J., Eitinger M., Friedrich B.;
"Analysis of a pleiotropic gene region involved in formatic
catalytically active hydrogenases in Alcaligenes eutrophus
Arch. Microbiol. 159:545-553(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alcaligenes eutrophus (Ralstonia eutropha).
Plasmid megaplasmid pHG1.
Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPB_ALCEU
                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                           EMBL; X70183; CAA49732.1; -.
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                                                                                                                                                                                                   InterPro; IPR004392; HypB.
InterPro; IPR002894; HypB_UreG.
Pf4m; PF01495; HypB_UreG; 1.
TIGRP0073; hypB; 2.
Metal-binding; Nickel; Plasmid.
SEQUENCE 361 AA; 38483 MW;
                                                                                                                      300
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                                                                                                          AAGAAAAT 307
                                                                                             AAGAAAAT 330
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8; Conserv
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344
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Conservative
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36421 MW;
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Last annotation updat
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%; Pred. No. 15;
0; Mismatches
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Pred. No.
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; AC37A4EF919B71B5 CRC64;
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o. 14;
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                                    367
                                                                                                                                                                  DB 1;
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trophus H16.";
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RESULT 34
MOC3_HUMAN
ID MOC3_H
AC 095396
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                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
probable tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase
(EC 2.1.1.61).
TRMU OR RV3024C OR MT3108 OR MTV012.39C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=H37RV;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium tuberculosis.
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STRAIN=CDC 1551 / Oshkosh;

Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Fleischmann R.D., Alland D., Eisen J.A., Haft D., Hickey E., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Salzberg Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg Belcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature [2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98295987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=1773;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                   EMBL; AL021287; CAA16109.1; -.
EMBL; AE007129; AAK47438.1; -.
TIGR; MT3108; -.
                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
                                                                                                                                                                                                                                      Transferase; Methyltransferase; tRNA processing; Complete SEQUENCE 367 AA; 38120 MW; 043ECC2D5D690C79 CRC64;
                                                                                                                                                                                                                                                                   InterPro; IPR004506; TrmU.
InterPro; IPR004135; tRNA_Me_t
InterPro; IPR004135; tRNA_Me_t
Pfam; PF03054; tRNA_Me_trans;
TIGRFAMS; TIGR00420; trmU; 1.
                                                                                                                                                                                                                                                                                                                                   TubercuList; Rv3024c;
                                                                                                  351 ATTAGASG
                                                                                                                                    59 ATIAGASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           thiouridylate.
                                                                                                                                                                    Similarity
8; Conserv
                                                                                                                                                                      Conservative
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Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=9634230;
                                                                                                                                                                                        1.6%;
                                                                                                                                                                           0;
                                                                                                                                                                                         Score 8;
Pred. No
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                         PRT;
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                                                                                                                                                                                                           DB 1;
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MOC3\_HUMAN 095396;

STANDARD;

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PSBO_EUGGR
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Best Local
                           protein of photosystem II in Eugle
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                                                                                                                                                                             PSBO
                                                                                                                                                                                         Oxygen-evolving enhancer protein
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01-FEB-1996 (Rel.
16-OCT-2001 (Rel.
                                                                                                                                                                                                                             P46483;
01-NOV-1995
                                                                                                                                                                                                                                                         PSBO_
                                                                                                                                                                                                                                                                                                                                                                                                                         Lipopolysaccharide biosynthesis; SEQUENCE 311 AA; 36730 MW; C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE000440; AAC76653.1; PIR; A42982; A42982.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Analysis of the Escherichia coli genome. V. region from 76.0 to 81.5 minutes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=K12 / MG1655;
MEDLINE=94316500; PubMed=8041620;
Sofia H.J., Burland V., Daniels D.L., Plunkett G. III, Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              core
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Structures of the rfaB, rfaI, rfaJ, and rfaS genes of Escherichia coli K-12 and their roles in assembly of the lipopolysaccharide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pradel E., Parker C.T., Schnaitman C.A., Structures of the rfaB, rfaI, rfaJ, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=92325066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lipopolysaccharide RFAS OR B3629.
Plant
                                                                          Shigemori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic Acids Res. 22:2576-2586(1994).
                                                              Shigemori Y., Yamamoto Y.;
                                                                                      MEDLINE=94154233;
                                                                                                                                     NCBI_TaxID=3039;
                      nydrophobic
                                                                                                                                                                                                                                                                                                                      191 KDKTSSTT 198
                                                                                                              EQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                               67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteriol. 174:4736-4745(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PATHWAY: Lipopolysaccharide core biosynthesis.
FUNCTION:
                                                                                                                                                                                                                                                                                                                                               KDKTSSTT
                                                                                                                                                                                                                                                         EUGGR
           Mol. Biol. 24:209-215(1994)
                                                                                                                                                                                                                                                                                                                                                                       Similarity
8; Conserv
                                                                                                                                                   Euglenozoa;
                      domains
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STABILIZES THE MANGANESE CLUSTER WHICH IS THE PRIMARY
                                                                         Inagaki J.,
                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                      40,
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                                                                                     PubMed=8111018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              core biosynthesis protein
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                                                                                                                                                                                      Last sequence update)
Last annotation update)
cer protein 1, chloroplast
                                                                                                                                                                                                                               Created)
                                                                                                                                                   Euglenida;
                                                                                                                                                                                                                                                                                                                                                                                                 . 68;
                                                                                                              SEQUENCE
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                                                                          Mori H.,
                                                                                                                                                                                                                                                                                                                                                                                   Score 8; |
Pred. No.
                                   Euglena
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                                   gracilis
                                                 the nucleus-encoded
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 31
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                                                                                                                                                                                                                Ouyen D.T., Schmidt-Dannert C., Schmid R.D.;

Ouyen D.T., Schmidt-Dannert C., Schmid R.D.;

Pilgh-level formation of active Pseudomonas cepacia lipase after heterologous expression of the encoding gene and its modified chaperone in Escherichia coli and rapid in vitro refolding.";

Appl. Environ. Microbiol. 65:787-794(1999).

-!- FUNCTION: SEEMS TO BE ACTING IN THE FOLDING OF THE EXTRACELLULAR LIPASE DURING ITS PASSAGE THROUGH THE PERIPLASM.

-!- SUBCELLULAR LOCATION: INNER-MEMBRANE ANCHORED (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE LIPASE CHAPERONE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con entitles requires a license agreement (See http://www.isb-sib.ch/ar or send an email to license@isb-sib.ch).
                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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16-OCT-2001 (Rel. 40, Last sequence update)
15-OUN-2002 (Rel. 41, Last annotation update)
Lipase chaperone (Lipase foldase) (Lipase helper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF01716; MSP; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation \cdot
             Lipid
                                          EMBL; AJ131766; CAA10510.1; -. InterPro; IPR004961; Lipase_chap.
                                                                                                                       the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99124623;
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-ATCC 21808;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Burkholderia
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Burkholderia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Photosynthesis; Photosystem II; Chloroplast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; D14702; BAA03529.2; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              with the photosystem II complex.
-!- SIMILARITY: BELONGS TO THE PSBO FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane; associated
                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIPB OR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
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             PF03280; Lipase_chap; degradation; Chaperon
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8; Conserv
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llarity 100.0%;
Conservative
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oteobacteria; beta subdivision;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein) (Lipase modulator).
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             Chaperone;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHLOROPLAST
             Transmembrane; Periplasmic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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HSSP; P06601; 1FJL.
TRANSFAC; T04038; -.
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MIM; 601845; -.
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01-NOV-1997
01-NOV-1997
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DOMACH
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HOMEOBOX.
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R -> C.
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SMART; SM00389; HOX; 1.
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                                                                                                                                                                                                                                                                                     Eukaryota; Euglenozoa;
NCBI_TaxID=3039;
                                                                                                                                                                                                         Deruere J., Schantz M.L., Schantz R.;
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE L10E FAMILY OF RIBOSOMAL PROTEINS
                                                                                                                                                                                                                                                                                                                  Euglena gracilis.
                                                                                                                                                                                                                                                                                                                                             60S ribosomal protein
                                                                                                                                                                                                                                                                                                                                                                                                                 RL10_EUGGR
             Interpro: IPR001197; Ribosomal_L10E.
pfam; pF00826; Ribosomal_L10e; 1.
TIGRFAMS; TIGR00279; L10e; 1.
pROSITE; PS01257; RIBOSOMAL_L10E; 1.
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SIMILARITY: BELONGS TO "BICOID" SUBFAMILY.
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ilarity 100.0%;
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(Rel. 35, Last sequence update)
(Rel. 35, Last annotation update)
al protein L10.
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665C33D9C454E7A7 CRC64;
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VG67_
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Equine herpesvirus type 1 (strain Ab4p) (EHV-1), and Equine herpesvirus type 1 (strain Kentucky A) (EHV-1). Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Alphaherpesvirinae; Varicellovirus.
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STRAIN=Kentucky A;
MEDLINE=93079867; PubMed=1333117;
MEDLINE=93079867; PubMed=1333117;
Breeden C.A., Yalamanchili R.R., Colle C.F. III, O'Callaghan D.J.;
I'dentification and transcriptional mapping of genes encoded at the
"Identification of equine herpesvirus type 1.";
IR/Us junction of equine herpesvirus type 1.";
  01-AUG-1992
01-AUG-1992
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M86664; AAB02512.1; EMBL; M86664; AAB02502.1; EMBL; M80429; AAA46076.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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P27126;
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PIR; B44215;
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(Rel.
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B44215.
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24, Last sequence update)
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67 protein (IR6 protein).
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23, Last sequence 41, Last annotations
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                                                                                                                                                                                                                                                                           Spermatophyta; Magnoliophyta; Ehrhartoideae; Oryzeae; Oryza
                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                          Oryza sativa (Rice)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                 SUBUNIT: V-ATPASE IS AN HETEROMULTIMERIC ENZYME COMPOSED OF PREIPHERAL CATALYTIC VI COMPLEX (MAIN COMPONENTS: SUBUNITS A C, D, E, AND F) ATTACHED TO AN INTEGRAL MEMBRANE VO PROTON F COMPLEX (MAIN COMPONENT: THE PROTEOLIPID PROTEIX; WHICH IS AS A HEXAMER THAT FORMS THE PROTON-CONDUCTING PORE).

SUBCELLOUAR LOCATION: Integral membrane protein. Vacuolar.
MISCELLANEOUS: THIS SUBUNIT BINDS DICKCHEXYLCARBODIIMIDE (WHICH INHIBITS THE ATPASE (BY SIMILARITY).
         European Bioinformatics Institute.
                                                                                                                                                        CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) =
                                                                                                                                                                   FOR ACIDIFYING A VARIETY OF INTRACELLULAR COMPARTMENTS EUKARYOTIC CELLS.
                                                                                                                                                H(+)(Out).
                                                                                                                                                                                       is (1995), Fudan University, China.
FUNCTION: PROTON-CONDUCTING PORE FORMING SUBUNIT OF THE MEMBRANE
INTEGRAL VO COMPLEX OF VACUOLAR ATPASE. V-ATPASE IS RESPONSIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                       GLAGLAAG
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                   SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EM
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InterPro; IPR000245; Vac_ATPsynt_Csub.
Pfam; PF00137; ATP-synt_C; 2.
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                                                                                                                                                                                                                                     homeodomain-containing gene VCFS/DGS on 22q11.";
                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
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30-MAY-2000 (Rel.
15-JUN-2002 (Rel.
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             -
                                                                                                                             development.";
                                                                                                                                                                 Roe B., Budarf M.L.;
                                                                                                                                                                              Gottlieb
                                                                                                                                                                                       MEDLINE=97294411;
                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                Funke B., St Jore B., Puech A., Sirotkin H., Edelmann L., Carlson C., Raft S., Pandita R.K., Kucherlapati R., Skoultchi A., Morrow B.E.; "Characterization and mutation analysis of goosecoid-like (GSCL), a homeodomain-containing gene that maps to the critical region for
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., MEDLINE=98110571; Pu
                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
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                                                                                                                                         "The DiGeorge syndrome minimal critical region like (GSCL) homeobox gene that is expressed ear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              103 GLAGLAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     282 GLAGLAAG
                                                                                           J. Hum. Genet. 60:1194-1201(1997).
FUNCTION: MAY HAVE A ROLE IN DEVELOPMENT. MAY REGULATE TRANSCRIPTION. MAY BIND THE BICOID CONSENSUS SEQUENCE
DEVELOPMENTAL STAGE: EXPRESSED IN EARLY HUMAN DEVELOPMENT AS AS IN A LIMITED NUMBER OF ADULT TISSUES.

DISEASE: HAY BE RELATED TO SOME OF THE DEVELOPMENTAL DEFECTS ASSOCIATED WITH VELOCARDIOFACIAL AND DIGEORGE SYNDROMES
                                                          SUBCELLULAR LOCATION: Nuclear (By similarity).
TISSUE SPECIFICITY: DETECTED IN ADULT TESTIS AND 9-10 WK FETAL TISSUE (THORAX). PROBABLY EXPRESSED
                                               AT LOW LEVELS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PR00122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
8; Conser
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                                                                                                                                                                              S., Emanuel
                                                                                                                                                                                                                           46:364-372(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGR01100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                          . 39, Created)
. 39, Last sequence update)
. 41, Last annotation update)
goosecoid-like (GSC-2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              statement
a license
                                                                                                                                                                           PubMed=9150167;
uel B.S., Drisco
                                                                                                                                                                                                                                                                                                PubMed=9441739;
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                                                                                                                                                                                                                                                                                                         AND VARIANT CYS-47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.6%;
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                                                                                                                                                                            Driscoll D.A.,
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DICYCLOHEXYLCARBODIIMIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
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                                                                                                                                                                              Sellinger
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SEQUENCE TAATCC.
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                                                                       PITUITARY,
                                                                                                                                           human
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                                    WELL
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RX MEDILINE-21849401; PubMed=11859360;
RA MEDILINE-21849401; PubMed=11859360;
RA Sgouros J., Peat N., Hayles J., Basham D., Bowman S.,
RA Sgouros J., Peat N., Hayles J., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Gentles S., World S., Horsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Monney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Monney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Monney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Skelton J., Vanstreels E., Airt R., Robben J., Grymonprez B.,
RA Moodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Moodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Meltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller Auer S.,
RA Meltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller S.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Beger P., Zimmermann W., Wedler H., Reinhardt R., Pohl T.M.,
RA Beger P., Zimmermann W., Wedler H., Reinhardt R., Pohl T.M.,
RA Beger P., Zimmermann W., Wedler H., Reinhardt R., Pohl T.M.,
RA Baga R.R., Cruzado L., Jimenez J., Sanchez M., Gerzon A., Thode G.,
RA Lucas M., Rochet M., Geillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., Gel Rey F., Benito J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT. Mathre Alfs. R371-R801/2012).
Br. Lather Alfs. R371-R801/2012).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P50515;
01-OCT-1996
01-OCT-1996
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schizosaccharomyces pombe (Fission yeast).
Eukaryota: Fungi: Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VMA3 OR SPAC1B3.14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                          "THE GENOME TO TAKE THE GENOME TO THE GENOME TO THE THE TENCTION: PROTON-CONDUCTING PORE FORMING SUBUNIT OF THE INTEGRAL VO COMPLEX OF VACUOLAR ATPASE. V-ATPASE IS RESPONDED ACTORITYING A VARIETY OF INTRACELLULAR COMPARTMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           royama R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=92206078; PubMed=1839480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=4896;
                                                                                                                                                                 This
                                      entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                           modified and this statement is not removed.
                                                                                                                      between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        yama R., Goldstein D.J., genomic sequence of the
                                                                                                                                                                                                      H(+)(Out).
SUBUNIT: V-ATPASE IS AN HETEROMULTIMERIC ENZYME COMPOSED OF A SUBUNIT: V-ATPASE IS AN HETEROMULTIMERIC ENZYME COMPOSED OF A PERIPHERAL CATALYTIC VI COMPLEX (MAIN COMPONENTS: SUBUNITS A, B COMPLEX (MAIN COMPONENT: THE PROTEOLIPID PROTEIN; WHICH IS PRESCRIBED AS A HEXAMARE THAT FORMS THE PROTEON-CONDUCTING PORE).

SUBCELLULAR LOCATION: Integral membrane protecin. Vacuolar. MISCELLANEOUS: THIS SUBUNIT BINDS DICYCLOHEXYLCARBODIMIDE (DCI WHICH INTEGRAL PROTEOLIPID SUBUNIT FAMILY.)

WHICH INHIBITS THE ATPASE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                FOR ACIDIFYING A VARIETY OF INTRACELLULAR COMEUNARYOTIC CELLS.

CATALYTIC ACTIVITY: ATP + H(2)0 + H(+)(In) =
                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7:989-991(1991).
                                                                                                       non-profit
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      CAA42572.1;
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34,
41,
                                                                                                         institutions as long
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Last annotation update)
16 kDa proteolipid subunit (EC:3.6.3.14).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
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Schizosaccharomyces pombe
                                                                                                       There are no restrictions ng as its content is in
                                                                  http://www.isb-sib
                                                                                 Usage
                                                                                                                                                and the
                                                                                                                                                                                                                                                                                                                                                                                                                       ADP
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RESULT 24
VATL_AVESA
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Best Local S
Matches 8
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01-MAR-1992
15-JUN-2002
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BINDING
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002379; ATPase_Csub.
InterPro; IPR000245; Vac_ATPsynt_Csub
pfam; PF00137; ATP-synt_C; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIGRFAMS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Z98598; CAB11240.1;
by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement or send an email to "14".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hydrolase;
                                                                                                                                                                                                                                                                                                          STRAIN=CV. LANG; PubMed=1831453; MEDLINE=91340758; PubMed=1831453; Lai S., Watson J.C., Hansen J.N., Sze H.; Lai S., Watson J.C., Hansen J.N., Sze H.; Molecular cloning and sequencing of cDNAs encoding subunit of the vacuolar H(+)-ATPase from a higher pl J. Biol. Chem. 266:16078-16084(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Avena sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vacuolar ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P23957;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VATL_AVESA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                      This
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                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                              Aveneae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                282 GLAGLAAG 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99
                                                                                                          SUBUNIT: V-ATPASE IS AN HETEROMULTIMERIC ENZYME COMPOSED OF PERIPHERAL CATALYTIC V1 COMPLEX (MAIN COMPONENTS: SUBUNITS PERIPHERAL CATALYTIC V1 COMPLEX (MAIN COMPONENTS: SUBUNITS POLICY (MAIN COMPONENT: THE PROTEOLIPID PROTEIN; WHICH IS POMBLEX (MAIN COMPONENT: THE PROTEON-CONDUCTING PORE).

AS A HEXAMER THAT FORMS THE PROTON-CONDUCTING PORE).

SUBCELLULAR LOCATION: Integral membrane protein. Vacuolar.

MISCELLANBOUS: THIS SUBUNIT BINDS DICYCLOHEXYLCARBODIMIDE (MISCELLANBOUS: THE ATPASE (BY SIMILARITY).

WHICH INHIBITS THE ATPASE (BY SIMILARITY).
                                                                                                                                                                                                                                                                           FUNCTION: PROTON-CONDUCTING PORE FORMING SUBMIT OF ITH
INTEGRAL VO COMPLEX OF VACUOLAR ATPASE: V-ATPASE IS RE-
FOR ACIDITYING A VARLETY OF INTRACELLULAR COMPARTMENTS
                                                                                                                                                                                                                                            EUKARYOTIC CELLS.

CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLAGLAAG
                                                                                                                                                                                                                                 H(+)(Out).
                                                                                                                                                                                                                                                                      FOR ACIDIFYING A VARIETY OF
                                                                        SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PR00122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                Avena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGR01100; V_ATP_synt_C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hydrogen ion transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              161 AA;
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33
76
72
114
126
152
138
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(Rel. 21, Last sequence update)
(Rel. 41, Last annotation update)
p synthase 16 kDa proteolipid subunit (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Oat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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113
125
151
161
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Pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DICYCLOHEXYLCARBODIIMIDE (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
LUMENAL (POTENTIAL)
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                                                                                                                                                                                                                                                                         INTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATP synthesis; Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              β
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 161;
                                                                                                                                                                                                                                                  ADP + phosphate
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plant.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAY-2000 (Rel.
30-MAY-2000 (Rel.
16-OCT-2001 (Rel.
Vacuolar ATP
                                                                                                                                                                                                                                                           EMBL; Y09572; CAA70764.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                     Fieschi F., Torrents E., Toulokhonova L., Jordan A., Hellman U., Barbe J., Gibert I., Karisson M., Sjoeberg B.M.; "The manganese-containing ribonucleotide reductase of Corynebacterium ammoniagenes is a class Ib enzyme.";
J. Biol. Chem. 273:4329-4337(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Corynebacterium ammoniagenes (Brevibacterium ammoniagenes). Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacteriaceae;
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069272;
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16 kDa proteolipid subunit (EC
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N-ACYL DIGLYCERIDE (POTENTIAL).
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RESULT 23
VATL_SCHPO
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Best Local
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Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: PROTON-CONDUCTING PORE FORMING SUBUNIT OF THE MEMBRANE
-INTEGRAL VO COMPLEX OF VACUOLAR ATPASE. V-ATPASE IS RESPONSIBLE
FOR ACIDITYING A VARIETY OF INTRACELLULAR COMPARTMENTS IN
                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (Some or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- SUBCELLULAR LOCATION: Integral membrane protein. Vacuolar.
-i- MISCELLANEOUS: THIS SUBUNIT BINDS DICYCLOHEXYLCARBODIIMIDE (DCD)
-WHICH INHIBITS THE ATPASE (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE V-ATPASE PROTEOLIPID SUBUNIT FAMILY.
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MEDLINE=93015814; PubMed=1400281;
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
                                                                                                             SEQUENCE
                                                                                                                             BINDING
                                                                                                                                          DOMAIN
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EMBL; AL451017; CAC18222.1;
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              282 GLAGLAAG
 99
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Bioenerg. Biomembr. 24:361-370(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H(+)(Out).
SUBUNIT: V-ATPASE IS AN HETEROMULTIMERIC ENZYME COMPOSED OF A SUBUNIT: V-ATPASE IS AN HETEROMULTIMERIC ENZYME COMPOSED OF A PERIPHERAL CATALYTIC V1 COMPLEX (MAIN COMPONENTS: SUBUNITS A, B, PERIPHERAL CATALYTIC V1 COMPONENTS: SUBUNITS AND FOOTON PORE COMPLEX (MAIN COMPONENT: THE PROTECLIPID PROTEIN: WHICH IS PRESENT AS A HEXAMER THAT FORMS THE PROTON-CONDUCTING PORE).
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                                                                   Score 8; |
Pred. No.
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CYTOPLASMIC (POTENTIAL).
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RESULT 18
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RESULT 19
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ID RLA3_T
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15-JUN-2002 (Rel. 41, Last annotation updats
60S acidic ribosomal protein P2 (Allergen
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Dothideomycetes et Chaetothyriomycetes incertae sec
Mycosphaerellaceae; mitosporic Mycosphaerellaceae;
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"A cDNA clone coding for a novel allergen, Cla h III, of
"herbarum identified as a ribosomal P2 protein.";
J. Immunol. 154:710-717(1995).
-i- PUNCTION: PLAYS AN IMPORTANT ROLE IN THE ELONGATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cladosporium herbarum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=95114396;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=29918;
                                                                                                                                                                                                                                                       RLA3_TRYCR P26795;
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Pfam; PF00428; 60s_ribosomal;
                                                                                                                                                  01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence upd
01-CCT-1996 (Rel. 34, Last annotation u
60S acidic ribosomal protein P2-B (P2B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X77253; CAA54470.1;
                                                                          Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                               SEQUENCE FROM N.A
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SIMILARITY: BELONGS TO THE L12P FAMILY OF RIBOSOMAL PROTICE
CAUTION: Two distinct proteins have been termed allergen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: P1 AND P2 EXIST AS DIMERS
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8; Conserv
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111 AA;
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11124 MW; 297FAll3FEBEDF89
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TO THE L12P FAMILY OF RIBOSOMAL PROTEINS.
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Best Local
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"Nucleotide sequence of a cDNA encoding another Trypanosoma cruzi
acidic ribosomal P2 type protein (TcP2b).";

nucleic Acids Res. 20:2893-2893(1992).

-i- FUNCTION: PLAX'S AN IMPORTANT ROLE IN THE ELONGATION STEP OF
PROTEIN SYNTHESIS.

-i- SUBUNIT: P1 AND P2 EXIST AS DIMERS AT THE LARGE RIBOSOMAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001
16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, x65065; CAA46198.1; -.
PIR; S22950; R6UT2B.
InterPro; IPR001813; 60s_ribosomal.
Pfam; PF00428; 60s_ribosomal; 1.
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                                                                                                                                                                                                                                                           MEDLINE-98196666; PubMed=9537320;
Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L. Graham D.E., Overbeek R., Snead M.A., Koller M., Aujay M., Hube. Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
"The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -
                                              the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               066867;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aquifex aeolicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical lipoprotein
                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Aquificae;
                                                                                                                                                                                                                        Nature 392:353-358(1998).
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         294 AAAAGGAA 301
 EMBL; AE000698; A PROSITE; PS00013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 AAAAGGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT
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8; Conser
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112 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
1 lipoprotein AQ_615 precursor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88
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                   AAC06830.1;
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Pred. No.
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OR MET-3 IS THE INITIATOR.
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PROKAR\_LIPOPROTEIN; 1.

В 20

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Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottler S.,
Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
"The genome sequence of Schizosaccharomyces pombe.";
Nature 415:871-880(2002).

-i- FUNCTION: PLAYS AN IMPORTANT ROLE IN THE ELONGATION STEP OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., James K., Jones M., Leather S., McDonald S., McLean J., James K., Jones M., Leather S., McDonald S., McLean J., Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., McLear J., Simport S., Seger K., Sharp S., Stelfor J., Simmonds M., Squares D., Seger K., Sharp S., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Stelfor J., Simmonds M., Squares R., Squares S., Stevens K., Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S Moodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Rieger M., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., Fried C., Holzer B., Michael H., Reinhardt R., Pohl T.M., Fried C., Holzer B., Melther H., Benhardt R., Pohl T.M., Fried C., Holzer B., Michael H., Reinhardt R., Pohl T.M., Fried C., Holzer B., Michael H., Reinhardt R., Pohl T.M., Fried C., Holzer B., Michael H., Reinhardt R., Pohl T.M., Fried C., Holzer B., Michael H., Reinhardt R., Pohl T.M., Fried C., Holzer B., Michael H., Reinhardt R., Pohl T.M., Fried C., Holzer B., Michael H., Reinhardt R., Pohl T.M., Fried C., Holzer B., Michael H., Bender M., Be
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RPP2B OR RPA4 OR SPBC23G7.15C.
Schizosaccharomyces pombe (Fission yeast).
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01-AUG-1990 (Rel. 15, Last sequence u)
15-JUN-2002 (Rel. 41, Last annotation
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EMBL; M33142; AAA35337.1;
                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                               use by non-profit institutions as long amodified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
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MEDLINE=90220620; PubMed=2325655;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MISCELLANEOUS: YEASTS CONTAIN 4 INDIVIDUAL SMALL RIBOSOMAL A PROTEINS (RPA) WHICH CAN BE CLASSIFIED INTO TWO COUPLES OF SIMILAR BUT NOT IDENTICAL SEQUENCES. EACH COUPLE IS DISTINCTLY RELATED TO ONE OF THE TWO A PROTEINS PRESENT IN MULTICELLULAR ORGANISMS.

MISCELLANEOUS: RPA3 AND RPA4 ARE ESSENTIAL FOR CELL SURVIVAL,
                                                                                                                                                                                                                                                           s SWISS-PROT entry is copyright. It is produced through a collaboration even the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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ell. Biol. 10:2341-2348(1990).
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ITY: ALL FOUR RPA SHOW 35% IDENTITY. RPA4
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01-APR-1988 (Rel. 07, Last sequence up
01-NOV-1997 (Rel. 35, Last annotation
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                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Molecular cloning and analysis of cDNA sequences for two ribosomal proteins from Artemia. The coordinate expression of genes for ribosomal proteins and elongation factor 1 during embryogenesis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea; Branchiopoda; Anostraca; Artemiidae; Artemia.
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                                                                                                       Pfam; PF00428; 60s_ribosomal;
                                                                                                                                             EMBL; X02632; CAA26479.1;
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-!- SIMILARITY: BELONGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Artemia.
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Lenstra J.A., Moeller W.;
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01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
01-AUG-1988 (Rel. 08, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
60S acidic ribosomal protein P2-alpha (A2) (L40C) (L12EI).
RPP2A OR RPA2 OR SPBPBB7.06.
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Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales; Schizosaccharomyc
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                                                                                                                                                                                                                                                                                                                                                     "Sequence of the cDNA for one acidic ribosomal protein "Sequence of the cDNA for one acidic ribosomal protein "sequence";
                                                                                                                                                                                                                                      MEDLINE=90220620;
Beltramo
                                                                                                                                                                                                                                                                                                                          Schizosaccharomyces pombe.";
Nucleic Acids Res. 15:9089-9089(1987).
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE=88067727; PubMed=3684587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                282 GLAGLAAG
MEDLINE=21848401; PubMed=11859360;
MEDLINE=21848401; PubMed=11859360;
Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
Brown D., Brown S., Chillingworth T., Churcher C.M.,
                                                                                                                                                             Beltrame M., Bianchi M.E.;
"A gene family for acidic ribosomal proteins in Schizosaccharomyces
"A gene family for acidic ribosomal proteins in Schizosaccharomyces
pombe: two essential and two nonessential genes.";
Mol. Cell. Biol. 10:2341-2348(1990).
                                                                                                                 SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
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X92374; CAA63118.1;
M95063; AAA18550.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLAGLAAG
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8; Conser
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11043 MW;
                                                                                                                                                                                                                                                         PubMed=2325655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LUMENAL (POTENTIAL).
DICYCLOHEXYLCARSODIMIDE (BY A -> P (IN REF. 1). CAA63119).
6B7518DD7A0FEB62 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
CYTOPLASMIC (POTENTIAL).
POTENTIAL.
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LUMENAL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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o. 5.1;
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RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Gobbe A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Goliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Sguares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottler S.,
RA Golfeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottler S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Cerrutti L., Lowe T., McComble W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Latter 415:871-880(2002).
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망
                                                                                                      Query Match
Best Local 9
                                                                                    Matches
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Mol. Gen. Genet. 191:519-524(1983).
-i- FUNCTION: PLAYS AN IMPORTANT ROLE IN THE ELONGATION STEP OF PROTEIN SYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=84038947; PubMed=6355773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                    pfam; PF00428; 60s_ribosomal; 1.
Ribosomal protein; Phosphorylati
SEQUENCE 110 AA; 11158 MW; 2
                                                                                                                                                                                                                                                                          EMBL; Y00466; CAA68528.1; -. EMBL; M33138; AAA35335.1; -. EMBL; AL032684; CAA21791.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: BELONGS TO THE L12P FAMILY OF RIBOSOMAL PROTEINS
                                                                                                                                                                                                                                                  EMBL; AL032684; CAA2.
PIR; B34715; R6BY22.
                                                                                                                                                                                                                                nterPro; IPR001813;
                                          294 AAAAGGAA
  76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MISCELLANEOUS: YEASTS CONTAIN 4 INDIVIDUAL SMALL RIBOSOMAL A PROTEINS (RPA) WHICH CAN BE CLASSIFIED INTO TWO COUPLES OF SIMI BUT NOT IDENTICAL SEQUENCES. EACH COUPLE IS DISTINCTLY RELATED ONE OF THE TWO A PROTEINS PRESENT IN MULTICELLULAR ORGANISMS. MISCELLANEOUS: RPA3 AND RPA4 ARE ESSENTIAL FOR CELL SURVIVAL, WHEREAS RPA1 AND RPA2 ARE NOT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: P1 AND P2 EXIST AS DIMERS AT THE LARGE RIBOSOMAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTM: PHOSPHORYLATED (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: ALL FOUR RPA SHOW 35% IDENTITY. RPA4 IS HIGHLY RELATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT
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    AAAAGGAA
                                                                                      Similarity
8; Conserv
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                                                                                        Conservative
                                              301
                                                                                                                                                                        Phosphorylation; Multigene family.
11158 MW; 2B465A46E51606FE CRC64;
                                                                                                            1.6%;
                                                                                                                                                                                                                                  60s_ribosomal.
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Pred. No.
                                                                                             Mismatches
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There are no restrictions
ong as its content is in
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                                                                                                        0;
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RESULT 16 RLA4\_SCHPO

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RA Addms M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Addms M.D., Celniker S.E., Hil P.W., Hoskins R.A., Galle R.F., Ra Amanatides P.G., Scherer S.E., Hil P.W., Hoskins R.A., Galle R.F., Ra Barndon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Ballew R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., RA Abril J.F., Agbayani A., An H.-J., Andrews-Ffannkoch C., Baldwin D., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Besson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S., RA Besson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Chandra I., RA Besson K.Y., Deng S., Mays A.D., Dew I., Dietz S.M., Charla I., K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Dieyam C., RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Dieyam C., RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Ra Nelson D.R., Nelson K.A., Nixon K., Dollard J., Wei M.-H., Merson D.R., Renington K.A., Nixon K., Dollard J., Wei S., Ecleb J.M., Ra Nelson D.R., Nelson K.A., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Sland M., V., Mobarry C., Morris J., Moshrefi A., Ra Abhue B.C., Sland-Klands J., Wannsham M., P., Santh T., Resee M.G., Ra Agng Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.M., Resee M.G., Shen H., Shue B.C., Sland M., Zhang G., Zhao Q., Zheng Y., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Free M., Rubin G.M., Zhang G., Zhao Q., Zheng L., Free M., Rubin G.M., Zhong W., Zhu X., Smith H.O., The Global R.A., Shue B.C., Shao Q., Zheng L., Free M., Rubin G.M., Zhong S., Zhao Q., Zheng L., Land C., Shao 
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cloned from Drosophila
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                                                                                                                                                                                  EMBL; U55321;
                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed
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FlyBase: FBgn0017561; Orkl.
InterPro; IPR003280; K+channel_pore.
InterPro; IPR001622; K+channel_pore.
InterPro; IPR000636; M+channel_nlg.
                                                                                                                                         EMBL; AE003484; AAF47972.1; -.
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CHANNELS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Integral membrane protein (PO) TISSUE SPECIFICITY: WIDESPREAD EXPRESSION IN ADULT, EXPRESSION IN MUSCLE, BRAIN AND OVARY. ALSO PRESENT
                                                                                                                                                                                                                                                                                                                                                                                               European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ON EXTERNAL POTASSIUM CONCENTRATION. ACTS AS AN OUTWARDLY RECTIFYING CHANNEL BUT AS EXTERNAL POTASSIUM LEVELS INCREASE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MISCELLANEOUS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RECTIFYING CHANNEL IS REVERSED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: BACKGROUND POTASSIUM CHANNEL. RECTIFICATION IS DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IN LARVA AND EMBRYO
                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation burpean Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                       license agreement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN FAMILY OF POTASSIUM
                                                                                                                                                                                                                                                                                       http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                        Usage
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RESULT 14
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Best Local
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15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Vacuolar ATP synthase 16 kDa proteolipid subunit
ATPase 16 kDa proteolipid subunit) (Fragment).
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DOMAIN
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC cl
Panicoideae; Andropogoneae; Zea.
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                                                                                                                                                                                                              Plant Physiol.
                                                                                                                                                                                                                                                                                      STRAIN=cv. B73; TI
MEDLINE=94105294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                        clones.
                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 52-109 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                               Viereck R., Kirsch M.,
                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=cv. Lixis;
MEDLINE=96197807;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Panicoideae; Andropogoneae; NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zea mays (Maize)
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                                                                                                                                                                                                                                                                 Thai H.,
                                                                                                                                                                                                                                                                             Keith C.S., Hoang
                                                                                                                                                                                                                                                                                                                                                       inhibition
                                                                                                                                                                                                                                                                                                                                                                 "Down-regulation of plant V-type H+ -ATPase genes after light-induced
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-76 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       294 AAAAGGAAG 302
                                                         AS A HEXAMER THAT FORMS THE PROTON-CONDUCTING PORE).
SUBCELLULAR LOCATION: Integral membrane protein. Vac
TISSUE SPECIFICITY: HIGH EXPRESSION IN THE MESOCOTY
                                                                                                           H(+)(Out).

SUBUNIT: V-ATPASE IS AN HETEROMULTIMERIC ENZYME COMPOSED OF A PERIPHERAL CATALYTIC VI COMPLEX (MAIN COMPONENTS: SUBUNITS A, C. D. E, AND F) ATTACHED TO AN INTEGRAL MEMBRANE VO PROTON POICE.
           GROWTH.
MISCELLANEOUS:
                                    DEVELOPMENTAL
                                                ETIOLATED
                                                                                               COMPLEX (MAIN COMPONENT: THE PROTEOLIPID PROTEIN; WHICH IS PRESENT
                                                                                                                                                             CATALYTIC ACTIVITY: ATP + H(2)0 +
                                                                                                                                                                         FOR ACIDIFYING A VARIETY OF INTRACELLULAR COMPARTMENTS EUKARYOTIC CELLS.
                                                                                                                                                                                                 IN Physiol. 101:329-332(1993).
FUNCTION: PROTON-CONDUCTING PORE FORMING SUBUNIT OF THE MEMBRANE INTEGRAL VO COMPLEX OF VACUOLAR ATPASE. V-ATPASE IS RESPONSIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                S., Hoang D.O., Barrett B.M., Feigelman B.,
Baysdorfer C.;
                                                                                                                                                                                                                                                     sequence
INHIBITS
                                                                                                                                                                                                                                                                                                                                           of growth.";
384:285-288(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1001
                                                SPECIFICITY: HIGH EXPRESSION IN THE FED SEEDLINGS COMPARED TO THE BASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transmembrane;
                                                                                                                                                                                                                                                                                      TISSUE=Leaf;
4; PubMed=8278499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ΑA;
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                                                                                                                                                                                                                                                    analysis
                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Coleoptile;
PubMed=8617373;
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27
111
140
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ATPASE
             SUBUNIT
                                      EXPRESSION
                                                                                                                                                                                                                                                   of 130 randomly selected
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CYTOPLASMIC
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Pred. No.
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SIMILARITY)
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             DICYCLOHEXYLCARBODIIMIDE (DCDD)
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SEQUENCE 782 AA;
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MEDLINE-95130069; PubMed-7829060;
Wydner K.S., Sechler J.L., Boyd C.D., Passmore H.C.;
"Use of an intron polymorphism to localize the tropoelastin
"Use of an intron polymorphism to localize conservation with
mouse chromosome 5 in a region of linkage conservation with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its type of the Buropean Bioinformatics institute. There are no restrictions on its type of the Buropean Bioinformatics in the Buropean Bioinformatics and the statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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STRAIN-BALB/C; TIS
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OXA_CORS1
Q46337;
01-NOV-1997
01-NOV-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Structural protein; Repeat; Signal; Connective SIGNAL 1 27 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
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PRINTS; PR01500; TROPOELASTIN
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Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinopycetales; Corynebacterineae; Corynebacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chlumsky L.J., Zhang L., Jorns M.S.;
Chlumsky L.J., Zhang L., Jorns M.S.;
Requence analysis of sarcosine oxidase and nearby genes reveals nonlogies with key enzymes of folate one-carbon metabolism.";
homologies with key enzymes of folate one-carbon metabolism.";
J. Biol. Chem. 270:18252-18259(1955).
J. Biol. Chem. 270:18252-18259(1955).
J. BIOL. CATALYZES THE OXIDATIVE DEMETHYLATION OF SARCOSINE YIELD GLYCINE, HYDROGEN PEROXIDE AND 5,10-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          subunit).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=95355441; PubMed=7543100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-P-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U23955; AAC43461.1;
InterPro; IPR002556; GCV_T.
InterPro; IPR000205; NAD_binding.
InterPro; IPR000205; NAD_byr_redox;
ProDom; PD000139; FAD_pyr_redox;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                       ORK1_DROME
Q94526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oxidoreductase; Flavoprotein; SEQUENCE 967 AA; 102767 MW
                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Open rectifier potassium channel protein 1 (Two
                                                                                                                                                                                                                                                                                                                                                                                                                                          DROME
                                                                                                                                            Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                        ORK1 OR CG1615
                                                                                                                                                                                                                                                                 channel Ork1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 434 GAAVGAAAA 442
MEDLINE=97075152; PubMed=8917578; Goldstein S.A.N., Price L.A., Ros
                                                   TISSUE-Larva;
                                                                       SEQUENCE FROM N.A.
                                                                                                                     NCBI_TaxID=7227;
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CATALYTIC ACTIVITY: Sarcosine +
formaldehyde + H(2)O(2).

COFACTOR: FAD.
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SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO THE GCVT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAAVGAAAA 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity
9; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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; Pred. No.
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; C5F8A61F021134E9 CRC64;
            Rosenthal D.N.,
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o. 4.1;
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                 Pausch M.H.;
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EMBL; J02717; AAA30503.1; -.
EMBL; K03505; AAA30505.1; -.
EMBL; K03506; AAA30506.1; -.
EMBL; K03506; AAA30706.1; -.
EMBL; J02855; AAA30776.1; -.
EMBL; M58652; AAA30519.2; -.
PIR; A26728; A26728.
PIR; B26728; B26728.
PIR; B26728; C26728.
InterPro; IPR003979; tropoelastin.
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Mammalia; Eutheria; Ce
Bovidae; Bovinae; Bos.
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the Euro
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Eukaryota; Metazoa;
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Yeh H., Anderson N., Ornstein-Goldstein N., Bashir M.M.
Rosenbloom J.C., Abrams W.R., Indik Z., Yoon K., Parks
                                SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Manohar A., Shi W., Anwar R.A.; "Partial characterization of bovine elastin gene; comparison with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=91234332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alternative splicing of elastin Biochemistry 28:2365-2370(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rosenbloom J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Nuchal
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     MOD_RES
                     CHAIN
                                                           Structural protein; Connective tissue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-27 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Structure of the bovine elastin gene
alternative splicing of elastin mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-27 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Raju K., Anwar R.A.;
Primary structures of bovine elastin
                                              Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biol. Chem. 262:5755-5762(1987).
                                                                                                                                                                                                                                                                                                                                   INTO AN EXTÉNSIBLE 3D NETWORK.
SUBCELLULAR MATRIX OF E
SUBCELLULAR MATRIX OF E
ALTERNATIVE PRODUCTS: 3 ISOFORMS; A (SHOWN HERE
PRODUCED BY ALTERNATIVE SPLICING.
PTM: THE CROSSLINKS ARE MADE OF DEAMINATED LYS.
                                                                                                                                                                                                                                                                sWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: THE POLYMERIC ELASTIN CHAINS ARE CROSS-LINKED TOGETHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          for human elastin."
                                                                                                                                                                                                                         s requires a license agreement (See http://www.isb-sib.ch/announce, an email to license@isb-sib.ch).
                                                                          PR01500; TROPOELASTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of cDNA clones
Ju,
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e splicing.
26
7 747
105
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       ELASTIN.
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MEDLINE-99319892; PubMed=10392721;
Bahr U., Springfeld C., Tidona C.A., Darai G.;
Bahr U., Springfeld C., Tidona C.A., Darai G.;
"Structural organization of a conserved gene cluster of Tupaia
"Structural organization of a conserved gene cluster of Tupaia
herpesvirus encoding the DNA polymerase, glycoprotein B, a probable
herpesvirus encoding the DNA polymerase, glycoprotein B, a probable
processing and transport protein, and the major DNA binding protein.";
Virus Res. 60:123-136(1999).

Virus Res. 60:123-136(1999).

TYPONDETION: THIS PROTEIN MAY AFFECT TRANSLOCATION OF THE VIRUS
-!- FUNCTION: THIS PROTEIN MAY AFFECT TRANSLOCATION OF THE VIRUS
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                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                  Betaherpesvirinae.
NCBI_TaxID=132678;
                                                                                                                                                                                                                                                                                                                                                                                 Herpesvirus tupaia (Strain Viruses; dsDNA viruses, no
                                                                                                                                                                                                                                                                                                                                                                                                                              Probable
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                           EMBL; AF084543; AAD42934.1;
InterPro; IPR000501;
Pfam; PF01366; PRTP;
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                                                                                                                                                                        SIMILARITY: BELONGS TO THE HERPESVIRUSES PRTP FAMILY.
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and transport protein.
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RNA stage; Herpesviridae;
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                                                                                                                                  It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      782 AA.
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Best Local S
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EMBL; U12421; AAA83252.1; -.
EMBL; 282214; CAB55884.1; -.
EMBL; 26001110; AAH01110.1; -.
PIR; S14257; S14257.
Genew; HGNC:1158; BZRP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between the Bioinformatics Institute. There are no restrictions on its the by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                    CRTI_STRGR STANDARD; PKT; 50, AA:
P54981; P72447;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Phytoene dehydrogenase (EC 1.14.99.-) (Phytoene
                                                                                   biosynthesis from Streptomyces griseus.";

Mol. Gen. Genet. 252:658-666(1996).

-i- FUNCTION: THIS ENZYME CONVERTS PHYTOENE INTO ZETA-CAROTENE VINTERMEDIARY OF PHYTOFLUENE BY THE SYMMETRICAL INTRODUCTION DOUBLE BONDS AT THE C-11 AND C-11' POSITIONS OF PHYTOENE.

-i- COPACTOR: FAD (PROBABLE).
                                                                                                                                                                                                                                                                                          CRTI OR CRTE.
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between
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use by
                                                                                                                                                  schumann G., Nurnberger H., Sandmann G., Kruegel H.J.; "Activation and analysis of cryptic ort genes for carotenoid biosynthesis from Streptomyces griseus.";
                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=JA3933;
                                                                                                                                                                                                                                    Actinomycetales;
NCBI_TaxID=1911;
                                                                                                                                                                                      MEDLINE=97074881; PubMed=8917308;
                                                                                                                                                                                                                                                                Bacteria; Actinobacteria;
                                                                                                                                                                                                                                                                          Streptomyces griseus.
                                                                                                                                                                                                                                                                                                                                                                                                                               117
                                                                                                                                                                                                                                                                                                                                                                                                                                                    302 GAAAATTVA 310
           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEMBRANE SEGMENTS M1, M2, AND M4 FROM SUBUNITS OF GABA(A)/BENZODIAZEPINE RECEPTOR FAMILY, RESPECTIVELY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109610;
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GAAAATTVA 125
                                                              PATHWAY: Carotenoid biosynthesis. SIMILARITY: BELONGS TO THE PHYTOENE DEHYDROGENASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR004307; TSPO_MBR.
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                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                    bacteria; Actinobacteria (class); Actinobacteridae; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18779 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.8%;
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TM2
TM3
TM4
TM5
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Pred. No.
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1AD741BF99AB92CD CRC64;
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Best Local S
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QΥ
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                                                  Query Matc
Best Local
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[P$497];

P$497];

01-OCT-1996 (Rel. 34, Created)

01-OCT-1996 (Rel. 34, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)

15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interpro; IPR002937; Amino_oxidase.
Interpro; IPR0002171; Bac_Phytoene_dh.
Interpro; IPR000205; NAD_binding.
Interpro; IPR000205; NAD_binding.
Pfam; PF01593; Amino_oxidase: 1.
PROSITE; PS00982; PHYTOENE_DH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; L37405; AAA91950.1; -. EMBL; X95596; CAA64850.1; -.
                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carotenoid biosynthesis; Oxidoreductase; FAD; Flavoprotein; NP_BIND 12 45 FAD (ADP PART) (POTENTIAL).
SEQUENCE 507 AA; 54509 MW; FBB97F7FE696B2AC CRC64;
                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptomyces setonii.
Bacteria; Actinobacteria;
                                                                                                                                                                                                                                                                                                                                                                                    + + +
                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: THIS ENZYME CONVERTS PHYTOENE INTO ZETA-CAROTENE VIA INTERMEDIARY OF PHYTOFLUENE BY THE SYMMETRICAL INTRODUCTION OF DOUBLE BONDS AT THE C-11 AND C-11' POSITIONS OF PHYTOENE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN-ISP 5395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=38315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 280 GAGLAGLAA
                                                                                                                                                                           InterPro; IPR002937; Amino_oxidase.
InterPro; IPR000171; Bac_phytoene_dh
InterPro; IPR000205; NAD_binding.
                                                                                                              pfam; pF01593; Amino_oxidase; 1.
pR0SITE; pS00982; pHYTOENE_DH; 1.
Carotenoid biosynthesis; Oxidoreductase; FAD;
CAP_BIND 12 45 FAD (ADP PART) (1)
NP_BIND 12
                                                                                                                                                                                                       EMBL; D55723; BAA09537.1; -
InterPro; IPR002937; Amino_
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                                                                                                  SEQUENCE
   280 GAGLAGLAA 288
                                                                  Match
                                                                                                                                                                                                                                                                                                                                                                              PATHWAY: Carotenoid biosynthesis.
SIMILARITY: BELONGS TO THE PHYTOENE DEHYDROGENASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                  COFACTOR: FAD (PROBABLE)
PATHWAY: Carotenoid bios
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9;
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                                   Similarity
9; Conserv
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                                                                                                   508 AA;
                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                     54610 MW;
                                                      1.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Actinobacteria (class); Actinobacteridae; ycineae; Streptomyces.
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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                                          Score 9; DB 1; Pred. No. 2.3
                                                                                                       4B6DEFC076D51CB5 CRC64;
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                                                         DB 1;
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                                                                                                                          (POTENTIAL).
                                                                            Length 508
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PKBS_HUMAN
ID PKBS_H
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DE Periph
GN BZRP OO
OS Homo s
OC Eukary
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RLA4_C
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Best Local
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                                                                                                                  PKBS_HUMAN STANDARD; PRT; 169 AA. p30536; Q96Tp6; 01-APR-1993 (Rel. 25, Created) 01-FEB-1994 (Rel. 28, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Peripheral-type benzodiazepine receptor (PBR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUN-2002
15-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Achatz G., Oberkofler H., Lechenauer E., Simon B., Unger A., Kandler D., Ebner C., Prillinger H., Kraft D., Breitenbach M., "Molecular cloning of major and minor allergens of Alternaria alternata and Cladosporium herbarum.";
Mol. Immunol. 32:213-227(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Fung1; Ascomycota; Pezizomycotina;
Dothideomycetes et Chaetothyriomycetes incertae sedis;
                          Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X78223; CAA55067.2; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycosphaerellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cladosporium herbarum
                                                   Homo sapiens (Human)
                                                                                                 benzodiazepine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=95206305; PubMed=7898496;
                                                                                                                                                                                                                                                                                                                                                                                                      293 GAAAAGGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTM: PHOSPHORYLATED (BY SIMILARITY).
SIMILARITY: BELONGS TO THE L12P FAMILY OF RIBOSOMAL PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEIN SYNTHESIS.
SUBUNIT: P1 AND P2 EXIST AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nitted (AUG-1999) to the EMBL/GenBank/DDBJ databases. FUNCTION: PLAYS AN IMPORTANT ROLE IN THE ELONGATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acidic
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                                                                           OR MBR
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                                                                                                                                                                                                                                                                                                                                                            GAAAAGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF00428; 60s_ribosomal;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein;
111 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ribosomal protein P2 (Minor allergen Cla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 32, Created)
(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                 receptor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 distinct proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phosphorylation;
11105 MW; C7B6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mitosporic Mycosphaerellaceae; Cladosporium
                        Chordata;
    Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60s_ribosomal.
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  Catarrhini;
                          Craniata;
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0.61;
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There are no rest
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RX MEDILINGE FROM N.A.

RA Dunham I., Hunt A.R., Collins J.E., Bruskiewich R., Beare D.M.,

RA Clamp M., Smink L.J., Alinscough R., Almeida J.P., Babbage A.K.,

RA Bagguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,

RA Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,

RA Clamp M., Smink L.J., Alinscough R., Almeida J.P., Chen Y., Clark G.,

Clay S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,

Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,

RA Clany D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,

RA Clay D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,

RA Dhami P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,

RA Hall R.E., Hall-Tamlyn G., Heathcott R.W., Ho S., Holmes S.,

RA Hall R.E., Hall-Tamlyn G., Heathcott R.W., Ho S., Holmes S.,

RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,

RA Martyn I.D., Masbreghi-Mohammadi M., Matthews L.H., Mccann O.T.,

RA McClay J., McLaren S., McMurray A.A., Milne S.A., Morthmore B.J., C.T.,

RA McClay J., McLaren S., McMurray A.A., Milne S.A., Morthmore B.J., C.T.,

RA McClay J., McLaren S., McMurray A.A., Milne S., Smatth M.L.,

RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,

RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,

RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,

RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,

RA Mincohima S., Kawasaki K., Sasaki Y., Aoki N., Mitsuyama S.,

RA ROB B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,

RA Mincohima S., John Y., Wang Z., White J., Wallianson D., Wu H., Vao Z.,

RA Alla R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,

RA Phan S., Olan Y., Rapt L., Ran Q., Shauli S., Sloan D., Song L.,

RA Phan S., Olan Y., Menis G., White J., Williams D., Wu H., Vao Z.,

RA Hall R., Wang Z., White J., Walder T., Pepin K., Nedson J.,

RA Williams A., Shiboso B., Wang S., Wang S., Walder S., Bedelmann L.,

RA Will
            <del>:</del> :
                                                                                                             Strausberg R.;
Submitted (DEC-2000) to
-!- FUNCTION: RESPONSIBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Molecular cloning and chromosomal localization of a human peripheral-type benzodiazepine receptor.";
Eur. J. Biochem. 195:305-311(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=91146565; PubMed=1847678; Riond J., Mattei M.-G., Kaghad M. Riong G., Caput D., Ferrara P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene
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                                                                                                                                                                       TISSUE=Lymph;
                                                                                                                                                                                          SEQUENCE FROM N.
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                                                                                                                                                                                                                                                                                         Wilkinson P.,
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PUNCTION: RESPONSIBLE FOR THE MANIFESTATION OF PERIPHERAL-TYPE BENZODIAZEPINE RECOGNITION SITES AND IS MOST LIKELY TO COMPRISE BINDING DOMAINS FOR BENZODIAZEPINES AND ISOQUINOLINE CARBOXAMID.

MAY PLAY A ROLE IN THE TRANSPORT OF PORPHYRINS AND HEME.

SUBCELLULAR LOCATION: MITOCHONDRIAL; INTEGRAL MEMBRANE DECERTIONS AND LARGE AND MEMBRANE DECERTION.
                                                                                                                                                                                                                                                  DNA sequence
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EMBL: M23222; AAA28541.1; ALT_TERM.
EMBL: M15762; AAA70424.1; -.
EMBL: M15763; AAA70423.1; -.
EMBL: M15764; AAA70423.1; -.
PIR; A43742; A43742.
HSSP: Q92831; 1B91.
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p13709; p13710;
01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
pemale sterile homeotic protein (Fragile-chorion FS(1)) OR FSH.
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Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    apparent membrane proteins.";

Dev. Biol. 134:246-257(1999).

-i- FUNCTION: REQUIRED MATERNALLY FOR PROPER EXPRESSION OF OTHER

-i- FUNCTION: REQUIRED MATERNALLY FOR PROPER EXPRESSION OF OTHER

HOMEOTIC GENES INVOLVED IN PATTERN FORMATION, SUCH AS UBX.

-i- SIMILARITY: HIGH, TO HUMAN RING3 PROTEIN.

-i- SIMILARITY: CONTAINS 2 BROWODOMAINS.
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MEDLINE=89276730: PubMed=2567251;
Haynes S.R., Mozer B.A., Bhatia-Dey N., Dawid I.B.;
"The Drosophila fsh locus, a maternal effect homeotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      293 GAAAAGGAAGA 303
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PROSITE; PS00633; BROMODOMAIN_1; 2.
PROSITE; PS50014; BROMODOMAIN_2; 2.
PROSITE; PS50014; BROMODOMAIN_2; 2.
PROSITE; PS50014; BROMODOMAIN_3; BROMODOMAIN_3; BROMODOMAIN_45 567 BROMODOMAIN_45 1106 ET DOMAIN_55 DOMAIN_55 1106
                                                                                                                                                                                                                                                                                                          FlyBase; FBgn0004656; fs(1)h.
InterPro; IPR001487; Bromodomain.
                                                                                                                                                                                                     PRINTS; PR00503; BROMODOMAIN. SMART; SM00297; BROMO; 2.
                                                                                                                                                                                                                                                                             Pfam; PF00439; bromodomain;
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                                                                                                                      Transmembrane; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
0.042;
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                         Query Match
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Matches
                                                                      EMBL; AP003001; BAB50082.1; -.
InterPro; IPR001911; Ribosomal_S21.
Pfan; PF00165; Ribosomal_S21; 1.
PRINTS; PR00976; RIBOSOMALS21.
PRINTS; PR00976; RIBOSOMALS21.
TIGRFAMS; TIGR00309; S21P; 1.
PROSITE; PS01181; RIBOSOMAL_S21; FALSE_NEG.
PROSITE; PS01181; RIBOSOMAL_S21; FALSE_NEG.
RIBOSOMAD PROTECTION COMPLETE PROTECTION.
SEQUENCE 88 AA; 10045 MW; 2C8536956D63215
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VARIANT
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
30S ribosomal protein S21.
RPSU OR MSR3117.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RS21_RHILO
                                                                                                                                                                                                                                                                                                                 watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Tabata S.;
Takeuchi C., Yamada M., Tabata S.;
"Complete genome structure of the
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=MAFF303099;
MEDLINE=21082930; PubMed=11214968;
                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between the Suropean Bioinformatics Institute. There are no restrictions on its the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rhizobium loti (Mesorhizobium loti)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            294 AAAAGGAAGAA 304
                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=381;
                                                                                                                                                                                                                                                                                            DNA Res.
                                                                                                                                                                                                                                                                                                     "Complete genome structure of the nitrogen-fixing Mesorhizobium loti.";
  296 AAGGAAGAA
                                                                                                                                                                                                                                                                               Res. 7:331-338(2000).
SIMILARITY: BELONGS TO THE S21P FAMILY OF RIBOSOMAL PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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451
750
790
816
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909
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2038
                                      Similarity
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                          Conservative
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                                                                             Complete proteome.
10045 MW; 2C8536956D632157 CRC64;
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Pred. No.
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                                0;
                                          Score 9;
Pred. No
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-> RKPYY
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                                Mismatches
                                              No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88
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0.11;
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                                   0;
                                                        Length 88;
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                                                                                                                                                                                                                                                                                                                         symbiotic bacterium
                                   Indels
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                                      Gaps
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15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
50S ribosomal protein L7/L12.
RPLL OR R01347 OR SMC01318.
Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Capela D., Barloy-Hubler F., Gouzy J., Bothe, G., Ampe F., Batut J., Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S., Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D., Portetelle D., Puehler A., Purnelle B., Ramsperger U., Renard C., Thebault P., Vandenbol M., Wedner S., Galibert F.; Analysis of the chromosome sequence of the legume symbiont Sinorhizobium meilloti strain 1021."; Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).

1- FUNCTION: Seems to be the binding site for several of the factor involved in protein synthesis and appears to be essential for a symbol of the control of the control of the synthesis and appears to be essential for a synthesis.
                                                                                                                                                                                                                                                                                              entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN-1021;
                                                                                                                                                                                         InterPro; IPR000206; Ribosomal_L12. Pfam; PF00542; Ribosomal_L12; 1. ProDom; PD001326; Ribosomal_L12; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21396507; PubMed=11481430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=382;
                                                                                                                                                                                                                                                                   EMBL; AL591787; CAC45926.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               accurate translation (By similarity).
SIMILARITY: BELONGS TO THE L12P FAMILY OF RIBOSOMAL PROTEINS.
                                                                Similarity
                                                                                                                              protein;
126 AA;
                                                                                                                                                                         TIGR00855; L12; 1.
                                          Conservative
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GALT_HUMAN
HI81_RHIME
HIS8_AGRT5
HIS8_BRUME
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FLGI_ZYMMO
SYW_METTH
WN16_HUMAN
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ELV3_MOUSE
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                                                             Score 11;
Pred. No.
                                                                                                                                71D2BF16FC487F88 CRC64;
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                                          Mismatches
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                                                             DB 1;
0.0096;
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08z386

Q91675

09167

092mg0

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RT "Cloning and nucleotide sequence of enzyme II of Brevibacterium
RT lactofermentum phosphotransferase system.";
RI lactofermentum phosphotransferase system.";
RI Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
C: FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENDLPYRUVATE-DEPENDENT
CC SUGAR PHOSPHOTRANSFERASE SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE
C SUGAR PHOSPHOTRANSFERASE SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE
C SUGAR PHOSPHOTRANSFERASE SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE
C AND THE TRANSPERANE CHANNEL; THE IIA DOMAIN COVTAINS THE PRIMARY
PHOSPHORYLATION SITE (THE DONOR IS PHOSPHO-HPR); IIA TRANSFERS IT TO
C PHOSPHORYL GROUP TO THE IIB DOMAIN WHICH FINALLY TRANSFERS IT TO
C THE SUGAR.
C -!- SUGALYTIC ACTIVITY: Protein N-phosphohistidine + sugar = protein
histidine + sugar phosphate.
C -!- SIMILARITY: CONTAINS 1 PTS EIIA DOMAIN.
C -!- SIMILARITY: CONTAINS 1 PTS EIIB DOMAIN.
C -!- SIMILARITY: CONTAINS 1 PTS EIIB DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Query Match Best Local S Matches 11

TIGRFAMs;

RESULT 1
RL7\_RHIME

RL7\_RHIME Q92QH8;

983 984 985 988 988 989 990 991 992 993 994 998 998

839 839 8410 8410 8410 8410 8410 8410 8410 8410
315 1 315 1 317 1
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CH16_DROGR
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YEYO_YEAST
EM12_PSEAE
PLAS_SILPR
NPM3_MOUSE
DHLE_RAPSA
RNFG_SALTI
Z137_HUMAN
NQRD_HAEIN
PCP_LACLC
VG32_BPML5
CDSN_PIG
HEXB_ADE02
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RLA2_ASPFU
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KPTA_DEIRA
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                                                                            AlaThrThrValAlaThrGlnIleThrValGlnAlaValValGlnAlaValLySGlnAla 325
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                                                    GCAGCAGCAGCAGCAGCATCG------GCAGCATTGGCAGCAGCAGCA 170
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0028I04"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert B. V
University of Utah (
University of Utah
Rm. 308, Biomedical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamii,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stop: 559
Location/Qualifiers
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Insert Length: 10000 Std Error: (
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Fax: 801 585 7177
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                with adaptors complementary to the insert adaptors and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="UUGC1M0539M10"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="Male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="E. Coli strain XL10-Gold, T1-resistant,
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1596	1537 GTCCAAATGGTAAAGAAAGAAGATGTCTCGGAGAGCAGCAGTGCAGAGCTGGACAGTGAC
297	297
297 1536	283 LeuAlaGlyLeuAlaAlaGlyAlaAlaValGlyAlaAlaAlaAla:
282 1476	267
266 1416	250 GluGlyThrMetAspThrValAsnThrValMetIleAlaValSerValAla
249 1356	230 AspLysGluArgGluGluTyrGlnGluMetLysAlaAlaGluGlnLysSerLysAspLeu :
229 1299	210 ThrGlnAlaGlnAlaAspGlnThrAsnLysLeuGlyLeuGluLysGlnAlaIleLysIle:
209 1245	190 AlaLysAlaIleGlnThrLeuGlyGluAlaThrLysSerAlaLeuSerAsnTyrAlaSer:::
189 1185	170 GluLeuProLysProGlyValThrProArgSerGluValIleGluIleGlyLeuAlaLeu : : : : : : : : : : : : : : : : : : :
169 1131	160SerSerGlySerAlaLysLeuGluThrPro:::::::
159 1071	151
150 1011	133 ThrLeuGluSerLeuGlnSerLeuSerAlaAlaGlnMetLysGluValGluAla:::    :::   :::
132 951	113 ThralaThrLysIlealaMetGlnThrSerIleGluGluAlaSerLysSerMetGluSer :
112 891	95 LysAlaGlyAlaAspThrGlyValSerGlyAlaAlaAlaThrThrAlaSerAsn :
94 831	83 GlyValAlaAlaGlyLysGluSerSerGluSerGln (
82 771	68
67 711	63 GlyAlaSerGlyLys
62 651	43 GlnIleGlnGlnThrArgGlnGlyLysAsnThrGluMetGluSerAspAlaThrIleAla ( :::
42 591	23 LeuThrSerThrProGlnGlyValProGlnGlnAspLysLeuSerGlyAsnGluThrLys ( :::   ::: 562 TCTGGGAAGTCACCCAAG
196	Z ARCAAGACGGTGAACTCTGTGTCGCACCCTGGGTCCGGAAAGACGGTGGTCCACCTGCTC

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	Fax: 801 585 7177 Email: ddunn@genetics.utah.edu		
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SLC, UT	Polymers Re		
	Unpublished (2000) Contact: Robert B. Weiss University of Utah Genome Center	JOURNAL COMMENT	COL
10kb	with paired end reads from	TITLE	
Reilly ern, A.	<pre>Dunn, D., Aoyagi, A., barber, M., beaccorn, T., buvai, B., hamili, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reil , M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, and Wright D. Weiss, R.</pre>	OTHORS	
e; Mus.	; Eutheria; Rodentia; Sciurognathi; s 1 to 526)	FERENCE	RE
stom1;	House muouse.  Mus musculus  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;	ORGANISM	ğ
	AZ312601.1 GI:10356717 GSS.	VERSION KEYWORDS	XE VE
genomic	1M0028I04R Mouse 10kb plasmid UUGC1M library Mus musculus clone UUGC1M0028I04 R, DNA sequence.	DEFINITION	DE DE
SEP-2000	AZ312601 526 bp DNA linear	RESULT 44 AZ312601 LOCUS	RE:
	GAGGAAG 2131	2125	Db
	aThrLys 471	469	QY
2124	CCTTCGGTCAAAGCTATGGCTCAGGAAGAACTCAGAGAGCCTCGAGGAGGACTCCAGCAGC	2065	Db
469		452	Qy
2064	CTCCAAGGGAAAGCTGCCTTGGGGCAAGGGGTGGCCCCAGTGCACACTCAGAAGACAGGG :	2005	Db
451		438	Qy
2004		1945	Db
438		426	Qy
1944		1894	Db
426	eMetGlnMetGlnLeuSerGluMetGlnGlnAsn-ValAlaGl	407	Qy
1893	ACCTCTTCAGCCAGCCTGTCATCCCCA	1867	Db
406		387	Qy
1866	ACCTCGTCCATTGTAAGGCAGGAGCGGTG	1837	DЬ
386	1	367	Qy
1836	:::	1777	дb
366		347	Оу
1776		1717	ДĎ
346		327	Оу
1716	GTGGCCACCCAGGTCAAGACTGACAGGGGCCAAAGGCCACTCAGGGAGCAGTGAGGAGTCA	1657	Db
326		318	Qy
1656		1597	Db
317	GlyalaalaGlyalaalaalaalaThrThrValalaThrGlnIleThrValGlnAla	298	Qy

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AUTHORS
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                                                               US-09-889-314-2 (1-496) x BC021514 (1-4088)
                                                                                                                                 Query Match:
                                                                                                                                                         Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                        Score:
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AsnMetSerIleSerSerSerSerGlyProAspAsnGlnLysAsnIleMetSerGlnVal
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BC021514
BC021514.1 GI:1
HTC.
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Contact: MGC help desk
Contact: Gapbs-r@mail.nih.gov
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BC021514 4088 bp mRNA linear HTC 07-AUG-2002 Mus musculus, Similar to Treacher Collins Franceschettl syndrome 1, homolog, clone IMAGE:5351783, mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (14-Jan-2002) National Institutes of Health Gene Collection (MGC), Cancer Genomics Office, Nation Institute, 31 Center Drive, Room 11A03, Bethesda, MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Haghsen, N., Ho, S.-L., Karlins, E., Kong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Tsurgeen, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone distribution: MGC clone distribution information can through the I.M.A.G.E. Consortium/LLNL at: http://lmage.lln Series: IRAK Plate: 55 Row: i Column: 23 This clone was selected for full length sequencing because passed the following selection criteria: matched mRNA gi: 6 This clone has the following problem: frame shifted.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
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                                                                                                                                                                                                                                                                                                                  /note="Vector: pCMV-SPORT6"
1210 c 1210 g 568 t
                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="NCI_CGAP_Mam6"
/lab host="ruior"
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                                                                                                                                                                                                                                                                                                                                                                  /lab_host="DH10B"
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{\tt rMetPheThrGlnPheTrpGlnGlnAlaSerLysIleAlaSerLysGlnThrGlyGluSe}
                                                 CCAGGTGTCGTGTCTGGAGAAGGAAACCAGTGAGCTCAAGGAGGCTATGGAA-----
                                                                                              nAsnValAlaGlnPheGlnLysGluValGlyLysLeuGlnAlaAlaAlaAspMetIleSe
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                                       ACAGGTACCACGCACAGCCACCACGGTCACCTCTAACATGAGCTCAAACCAAGACCCT
                                                                         SerGlyLysAspLysThrSerSerThrThrLysThrGluThrAlaProGlnGlnGly---
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This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing droup at the Stanford Human Center, Stanford University School of Medicine, Stanford Center, Stanford University School of Medicine, Stanford, Web site: http://www-shgc.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (03-JNN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
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Mammalia; Eutheria;
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969 c 813 g 810 t
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/clone_lib="NIH_MGC_94"
                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:10090"
/clone="IMAGE:4502186"
                                                                                                                                                                                                                                                                                                                                                              /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
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M., Schmutz, J., Grimwood, J., Rodriquez,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (18-AUG-2000) Yoshihide Hayashizaki, The Institute of physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Functional annotation of a full-length mouse cDNA collection Nature 409 (6821), 685-690 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
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   homolog
                                                                           /dev_stage="8 days embryo" <1. .2614
                                                                                                                                                                                                                               /strain="C57BL/6J"
/db_xref="FANTOM_DB:5730465C04"
/db_xref="MGD:MGI:1912849"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                   /note="data source:SPTR, source key:075300, evidence:ISS
                                                                                                                                                   /clone_lib="RIKEN full-length enriched mouse cDNA library"
                                                                                                                                                                                           /clone="5730465C04"
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COMMENT

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US-09-889-314-2 (1-496) x AK019964 (1-3110)
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                                                        122 SerIleGluGluAlaSerLysSerMetGluSerThrLeuGluSerLeuGlnSerLeuSer 141
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TLEPSMDIVLKLREAEETQNSLQAECDQYRTILAETEGMLKDLQKSVEEEEERVWKAKV
GAAEEELHKSRVTVKHLEDIVEKLKGELESSDQVREHTSHLEAELEKHMAAASAECQN
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QTRLKELESQVSCLEKETSELKEAMEQQKGKNNDLREKNWKAMEALALAERACEEKLR
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LNQATSQVESKQNTELAKLRQELSKVNKELVEKSEASRQEEQQRKALEAKAATFEKQV
LQLQASHKESEEALQKRLEEVTRELCRAQTSHANLRADAEKAQEQQQRVAELHSKLQS
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/translation="ASNQNRKTDTVANQGTKQEGVSNQVKKSEGSPNQGKKAEGAPNQ
GKKKDGSPSQAKKVDAAANQGKKSEMAPAQGQKASMVQSQEAPKQDAPAKKKSGSBKK
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/db_xref="GI:12860388"
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                                                                                                                                                                                               ACAGGGACAGCTACAGCAGCAACTATTGCTGCAGCAGCAACAGGCACAGTTGCAGCAGCA 331
                                                                                                                                                                                                                                                                          GCAGCAGCAGGACAGTTGCAACAGCAACACTTACAGCAGCAGGTACTGGTGCTGCAGCC
  LysAlaIleAlaLysAlaIleSerLysGlyIleSer---LysValPheAlaLysGlyThr 373
                                        GTTGCAGCAGCAGTTATGGCAACAGCAGCAGGAACAGTTGCAGCAGCAGCAGTTATTGCA 451
                                                                            IleLysAlaAlaVal------LysSerGlyIleLysAlaPheIleLysThrLeuVal 354
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1 (bases 1 to 786)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Plate: LLAM11109 row: b column:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                    -GlyAlaAlaAlaThrThrValAlaThrGlnIleThrValGlnAlaValValGln
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

205 c 238 g 102 t
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/clone_lib="NCI_CGAP_Lu29"
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/strain="CZECH II"
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Kawai, J., Sh
Arakawa, T.,
Aizawa, K., I
                                                                                                           Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Haradda, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGCAGCTCTGACTCAGATAGTTCCAGCAGTGAA---GAGGAGGAGAAGACTCCTAAGCCC
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                                                                                                                                                                                                                                                                                                         MetLysAlaAlaGluGlnLysSerLys
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Mus musculus
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                                                               GluGlnLysSerLysAspLeuGluGlyThrMetAspThrValAsnThrValMetIleAla
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 ValSerValAlaIleThrValIleSerIleValAlaAlaIlePheThrCysGlyAlaGly
                                                                                                                           LysGlnAlaIleLysIleAsp---LysGluArgGluGluTyrGlnGluMetLysAlaAla
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Mapping Project 337 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new operations.
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Mus musculus 14, 17 days embryo head cDNA, RIKEN full-length enriched library, clone:3233402K17:nucleolar and coiled-body
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20499374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              {\tt ThrIleAlaGlyAlaSerGlyLysAspLysThrSerSerThrThrLysThrGluThrAlam}
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{\tt LysAspLeuGluGlyThrMetAspThrValAsnThrValMetIleAlaValSerValAla}
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CAGAGTGGGTCACCTAAAAAGGGTGCTCTGGAAGGT---TCTTCAGGCTCAGCCTCTCAG
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                                                                       IleLysIleAspLysGluArgGluGluTyrGlnGluMetLysAlaAlaGluGlnLysSer
                                                                                                            AAATCTAGTTCAGAGGCAAACATTTCATCATCA---
                                                                                                                                               TyrAlaSerThrGlnAlaGlnAlaAspGlnThrAsnLysLeuGlyLeuGluLysGlnAla
                                                                                                                                                                                    {\tt TTGCCATTACTG---TCTTGTAAGTCTAGTTCAGAGACAGCTTCCAGTGGGTTAACATCT}
                                                                                                                                                                                                                         LeuAlaLeuAlaLysAlaIleGlnThrLeuGlyGluAlaThrLysSerAlaLeuSerAsn
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/db_xref="MGD:MGI:1918175"
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/clone_lib="RIKEN full-length enriched mouse
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1 (bases 1 to 1792)
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                                                                                                      Submitted (25-APR-2002) Maize Missouri, Columbia, MO 65211, Location/Qualifiers
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Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Yumamoto, R., Toue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y., Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control 
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                                                                                                                                                                                                                   with BamHI and XhoI. cDNA of size comprised longer than 7 kb was selected before cloning. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: Sall; 3' end: RamHI ucet. Duine
                                                                                                                                                                                                                                                                                                                                                        Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome-gsc.riken.go.jp/, Tel:81-45-503-9212, Fax:81-45-503-9216)
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Hume,D., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kosukawa,T.,
Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S.,
Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K.,
Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Quackenbush,J.,
Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
Schrinl,L., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T.,
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Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C.,
Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T.,
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Arakawa, T., Hara,
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Tissue Procurement: Gilbert Smith,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
Contact: Robert Strausberg, Ph.D
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National Institutes of Health, M
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Clone distribution: MGC clone distribution information
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                                                                                                                                                                                                                                                                                                                                                                                                        /note="organ: mammary; Vector: pCMV-SPORT6; Site_1: Sa:
site_2: NotI; Cloned unidirectionally. Primer: Oligo of
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
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/dev_stage="10 months, virgin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="IMAGE:4483398"
/clone_lib="NCI_CGAP_Mam1"
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/db_xref="taxon:10090"
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Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
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National Institutes of Health, Mammalian
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone='IMAGE:4748097"
/clone_Lib="NCI_CGAP_Skn4"
/tissue_type="squamous cell carcinoma"
/lab_host="bH10B ('Il phage resistant)"
/note="organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
/note="organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: SalI; Cloned unidirectionally. Primer: Oligo of Average insert size 1.5kb. Library constructed by Li
Technologies. Note: this is a NCI_CGAP Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anderson,O.D., Chao,S., Chin,A., Close,T.J., Gustafs,G.R., Rausch,C.J., Ross,K., Seaton,C.L. and Wilson, The structure and function of the expressed portion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldea; Triticeae; Triticem.
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Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WHE2911_D01_H01ZS Wheat aluminum-stressed root tip cDNA library Triticum aestivum cDNA clone WHE2911_D01_H01, mRNA sequence. BQ838510
                                                                                                                                                                                                                                                                                                                          Email: oandersn@pw.usda.gov
Sequences have been trimmed
                                                                                                                                                                                                                                                                                                                                                                                  West Area, Western Regional Research Center 800 Buchanan Street, Albany, CA 94710, USA Tel: 5105595773
                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Olin Anderson
US Department of Agriculture,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genomes - Aluminum
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                                                                                                                                                                                                                                                                                                     quality sequence with phred
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    Aluminum-stressed

/note-"Vector: Lambda Uni-ZAP XR, excised phagemid; Site_1: ECOR1; Site_2: XhoI; Plants were grown under hydroponic conditions, root tips were excised and sna frozen, total RNA was prepared at University of
                                                                                                 /clone_lib="Wheat aluminum-stressed root tip cDNA library"
/tissue_type="Root tip at 1.0 to 1.5 mm stage"
/dev_stage="Seedling"
                                                                                                                                                              /clone="WHE2911_D01_H01"
                                                                                                                                                                               /cultivar="BH1146"
/db_xref="taxon:4565"
                                                                                                                                                                                                                          /organism="Triticum
                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                   /lab_host="E. coli SOLR"
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Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadaceae; Chlamydomonas.

1 (bases 1 to 494)

1 (bases 1 to 494)

1 (system of the Chlamydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in Vascular Plants
                                                                                                                                                                      AW660984 11 C. reinhardtii CC-125 nutrient replete, 5. Fe Lambda 2ap II Chlamydomonas reinhardtii cDNA, mRNA sequence
                                                                                                       Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii
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Contact: Elizabeth
DCMB Box 91000
                                                       sAlalleSerLysGly
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Durham, NC 27708-1000,
Tel: 919 613 8164
Fax: 919 613 8177
TGCGACAATGGCGGGC
                                                                                                                            AGGAGCCATCAAG--
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- S for 2 hr), and iron-deprived cells from CC-125.
- S for 2 hr), and iron-deprived cells from CC-125.
- S for 2 hr), and iron-deprived cells from CC-125.
- S GII medium, as hit sGII -Fe
SGII medium at 0.18 micromolar Fe, 2x wash with SGII -Fe
sand resuspension in SGII -Fe + 80 micromolar
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/strain="CC-125 wild type mt+ 137C"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-125 nutrient replete,
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BE585195 773 bp mRNA linear EST 9-9H-ZO PsojaeZO Phytophthora sojae cDNA, mRNA sequence.
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                                                                                                                                                                                                                                                                                                   AGAACATCCGTCACTGAAGCTACACTAGTGGCGGCAGGAACCTCCGTTGAAGTCGCAATC 616
                                                                                                                                                                                                                 GTTGCTACCGGCGCGTCTGTCGCCGGAGCCTCGNACGTACTTGCTGGAGTCGTAGCCACT
                                                                                                                                                                                                                                                  GluSerSerGluSerGlnLysAlaGlyAlaAspThrGlyValSerGlyAlaAlaAlaThr 108
                                                                                                                                                       ThralaSerAsnThr---AlaThrLysIleAlaMetGlnThrSerIleGluGluAlaSer 127
ValGluAlaValValAlaAlaLeuSerGlyLysSerSerGlySerAlaLysLeuGlu
                                          GATGTGGTGGCTGGA-----AATTCCGTCGGAGTTGGATTCGTTGCTACTGGTGCTTCT 442
                                                                                  LysSerMetGluSerThrLeuGluSerLeuGlnSerLeuSerAlaAlaGlnMetLysGlu 147
                                                                                                                               GGTGCGTCTGTCACTGGAGCCNCGGCGGTTGTAGCTGGAGCATCCGTCACTGGAGTTTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Comparative analysis of expressed sequences in Plant Physiol. 123 (1), 243-254 (2000)
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pBK-CMV; Site_1: ECORI; Site_2: XhoI; This CDNA ilbrary was constructed from polyA+ enriched mRNA from zoospores grown in liquid medium. Zoospores were released into water and collected by centrifugation at 2,000g; zoospore-bearing sporangia were induced to develop on 5 to 7 d old mycelium colonies grown on VB agar by repeated flooding with water. Complementary DNA was synthesized from mRNA using an XhoI-poly(dT) linker-primer. ECORI adapters were ligated to the blunt-ended CDNA fragments and the products were digested
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/db_xref="taxon:67593"
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/lab_host="E. coli strain XLOLR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGAAGAGGCACT
                                                                                                                                               Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hgmp.mrc.ac.uk Vector: pBluescript II KS
V_type: phagemid
PRIMER: KS
                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Takifugu.

1 (bases 1 to 619)
Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umrania,Y., Williams,G., and Brenner,S.
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                                        /organism="Takifugu rubripes"
/db_xref="taxon:31033"
/clone="133B16aC7"
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                 /clone_lib="cosmid
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                                                                                                                                                                                                        Celera Genomics
45 w. Gude Dr.,
Tel: 2404533151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BM588321 711 bp mRNA linear EST 25-17000687322518 A.Gam.ad.cDNA.blood1 Anopheles gambiae cDNA-19600449697628 5', mRNA sequence.
                                                                                                                                                                                                                                                                                             1 (bases 1 to 711)
Holt.R.A., Lin.J.-J., Murphy,S.D., Evans,C.A.,
R., Collins,F.H., Venter,J.C. and Hoffman,S.L
Celera Anopheles gambiae EST project
                                                                                                                                                    Email: HoltRA@celera.com Plate: NU01004AAR row: F
                                                                                                                                                                                                                                                           Unpublished (2002)
Contact: Holt R.A.
                                                                                                                                                                                                                                                                                                                                                                                               Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                 African malaria mosquito
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                                                   /organism="Anopheles
/strain="RSP-ST (Redu
chromosome)"
                                                                                                                      Location/Qualifiers
/clone="19600449697628"
/clone_lib="A.Gam.ad.cDNA.blood1"
                                /db_xref="taxon:7165"
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                                       nAlaIleThrAlaAlaIleLysAlaAlaValLysSerGly 345
                                                                                                                         nIleThrValGlnAlaValValGlnAlaValLysGlnAlaValIleThrAlaValArgGl
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GGCTCTGGAGGCGGCGGCGGCGGCAGCTCTGGCGGCCGGG
                                                                                                                                                                     GGTGGCGGCGGCGGCGTGGCAGCTATGGCTCCGGAGGTGGCAGCTATGGCTCTGGA
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GCCTCTGAAAAAATTCTCCAGGTCAGAGCTGCCTCAGCCCCTGCCAAG-----
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                                                                                                                                                                                                                                 ---GCAAGAAAGGCGGCCCAGCCCTGGGAAGGTG---GGGGATGTGACACCCCAGGTC
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                                    ProGlnGlnGlyValAlaAlaGlyLysGluSerSerGluSerGlnLysAlaGlyAlaAsp 99
                                                                                                                                                     AAAGGAGGGCCCTGCCCCCAGCCAAGAGGGCCCAAGAAGCCCAGAAGAGGAGTCAGAGAGT
                                                                                                                                                                                                                                                                    {\tt SerThrProGlnGlyValProGlnGlnAspLysLeuSerGlyAsnGluThrLysGlnIle}
                                                                                                                                                                                                                                                                                                              TCAGTTTCTACTAAGGAGTCTCCA------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stop: 614.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:9606"
/clone="nMAGE:5737735"
/clone="lib="NLH_MGC_88".
/tissue_type="duodenal adenocarcinoma, cell line"
/tab_host="pH10B (phage-resistant)"
/note="Organ: small intestine; Vector: pCMV-SPORT6;
Site_1: Not1; Site_2: Sal1; Cloned unidirectionally;
oligo-dT primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH_MGC Library."
52 a 284 c 355 g 107 t 2 others
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                                                                       Takifugu rubripes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Takifugu.
1 (bases 1 to 443)
Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umrania,Y.,
Williams,G. and Brenner,S.
                                                                                                                                                                                               292062.1 GI:1869276
GSS; genome survey sequence
Takifugu rubripes.
Vector:
V_type:
        Submitted (18-FEB-1997) MRC Human Genome Mapping Project Resource Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hgmp.mrc.ac.uk Vector: pBluescript II KS
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DESCR:
One pass dye-terminator sequencing
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602659426F1 NCI_CGAP_Skn3 Homo s
                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) D
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                           Plate: LLAM10697 row: c column:
High quality sequence stop: 751.
Location/Qualifiers
                                                                                                                                                                                                                       Unpublished (1999)
                                                                                                                                                                                                                                            NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
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/clone="190022bB9"
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                           Direct Submission
Submitted (01-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                               Strausberg, R
                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                        Homo sapiens.
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                                                                                                                                                                                                                                                                                  1745 bp
clone IMAGE:3830953,
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mRNA
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                     AGCCCAAGTGCCCTGAATTCTCCAGGAATTGAG----
                                                      ThrProGlu----LeuProLysProGlyValThrProArgSerGluValIleGluIleGly
                                                                                             CCACTTTTAGAGAAGTGGCTAAATGATGCAGAGAACCTCTCATCTGATTCGTCCCTCTCC 822
                                                                                                                              AlaValValAlaAlaLeuSerGlyLysSer----SerGlySerAlaLysLeuGlu
                                                                                                                                                                   ACCATCTCTCGATTTGAAGCCTTG----AACCTCAGCTTTAAGAACATGTGCAAGTTGAAG
                                                                                                                                                                                                    MetGluSerThrLeuGluSerLeuGlnSerLeuSerAlaAlaGlnMetLysGluValGlu
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                                                                                                                                                                                                                                                                                ---GlnThrSerIle----
                                                                                                                                                                                                                                                                                                                   CTTGAGGAGCTTGAGCAGTTTGCCAAGACCTTCAAACAAGACGAATCAAACTTGGATTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 24 Row: d Column: 4
This clone has the following problem: frame shifted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortion
DNA Sequencing by: Institute for Systems Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clone distribution:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: MGC help desk
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/clone_lib="NIH_MGC_20"
/lab_host="DH10B-R"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
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Conservative:
Mismatches:
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Gaps:
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SCORES:  0.0129 Length: 130.50 Matches: 74 Similarity: 33.498 Mismatches: 159 Length: 1101 130.50 Conservative: 74 Conservative: 74 Similarity: 33.498 Mismatches: 159 Lilli: 117 Matches: 159 Lilli: 118 Spilsmilarity: 33.498 Mismatches: 159 Lilli: 119 ProfincincipyalasergiptysasplysthreserserthrithtysThredurthrala 77 Lilli: 110 Profincincipyalalalaigiptys	925	:::    GCAGCTAAAGCTGC		  GTAAACC	5 €	:::    CAAAGCTAA <i>I</i>	6	Db
SCOTES:  10.0129  130.50  130.	334	AlaValArgGlnAlaIle	nAlaValIleThr	ıValLysGl	ValG	ValGlnAlaVal	315	Qy
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ESCOTES:  10.0129  Length: 1101  130.50  Matches: 74  Conservative: 45  11 Similarity: 37.78%  Conservative: 45  11 Similarity: 37.78%  Conservative: 45  11 Similarity: 37.78%  Conservative: 45  11 Indels: 159  12 ACATTCAAAAACTGCTGCTTCAAAGAAACAAACAAACAAA	7	aIle	aIleThrValIle	SerValAl	IleAlaVal	ດ	257	Qy
ESCOTES:  10.0129  Length:  1101  130.30  Matches:  74  Conservative: 45  Isimilarity: 37.788  Conservative: 45  Isimilarity: 37.788  Conservative: 45  Isimilarity: 37.788  Conservative: 45  Isimilarity: 37.788  Conservative: 45  Indels: 159  177  ThrileAlaGlyAlaSerGlyLySASpLySThrSerSerThrThrLySThrGluThrAla 7  Illili:::::   ::   :     2 ACCATTCAGAGAGCAGTTCAGAGGACGAGGCTCCAGCAAAGCTGCCGGAAAGCTGCCTGC	700	ഹ –	AGAGGATGAAGAA	TCCTCTTC	GATTCAGAC	C	641	Db
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The second state of the se	640	₽	TGCTCCTGCA	GCTAAAGC	GCTGCTGC	CCTGCTACTAAG	581	Дb
TrilealaglyAlaserGlyLysAspLysThrEachashagChaagCcaanCTTGaa  Caccacagacacacacacacacacacacacacacacacac	242	•	uGluTyrGlnGlu	GluArgGl	IleAspLys	GlnAlaIleLys	225	Qy
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T 318 a 313 c 257 g 204 t 9 others    Scores   0.0129	224		aAspGlnThrAsn	AlaGlnAl	SerThrGlr	SerAsnTyrAla	205	Qy
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T 318 a 313 c 257 g 204 t 9 others    Scores:	241	AAATCTGTG	 AGCAACTGCAAAA	GAGGAAGC <i>I</i>	TCCTCTGAA	Ã	182	Db
T 318 a 313 c 257 g 204 t 9 others    Scores	0	SerGlyAla	sAlaGlyAlaAsp	SerGlnLys	SerSerGlu	}	89	Qy
VT 318 a 313 c 257 g 204 t 9 others    Scores:	œ	AG	TCCCGCAAAGAAA	TCCAAACG	GCAGCTGCT	C	122	фđ
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9 LysThrSerSerThrThrLysThrGluThrAlaProGlnGlnGlyValAlaAlaGlyLys 88	9 GlnGlyLysAsnThrGluMetGluSerAspAlaThrIleAlaGlyAlaSerGlyLysAsp 68 :::	9 GlyValProGlnGlnAspLySLeuSerGlyAsnGluThrLySGlnIleGlnGlnThrArg 48	9 SerSerGlyProAspAsnGlnLysAsnIleMetSerGlnValLeuThrSerThrProGln 28 	9-314-2 (1-496) x BQ735450 (1-887)	No.:       0.0107       Length:       887         No.:       130.00       Matches:       76         it Similarity:       37.69%       Conservative:       51         ocal Similarity:       22.55%       Mismatches:       126         Match:       5.49%       Indels:       84         Match:       14       Gaps:       12	238 a ,	/or /dr /dr /dr /dr /fe	Clone distribution: NCI-CGAP clone distribution: NCI-CGAP clone distribution: NCI-CGAP clone distribution of the Lamber of the L	Email: cgapbs-r@mail.nin.gov Tissue Procurement: Dr. Igor Dawid CDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation	Unpublish Contact:	E 1 (bases 1 to 887)  S NCI-CGAP http://www.nobi.nlm.nih.gov/ncicgap.  National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index	African c Xenopus 1 Eukaryota Amphibia;	IMAGE:5570055 5', mRNA sequence. B0735450 B0735450.1 GI:21874347 EST.	BQ735450 AGENCOURT 81488	ThrAlaAlaTleLysAlaAlaValLysSerGlyTleLysAlaPhe 349

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2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail:
seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and Yarrowia lipplytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.
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                                       GlnMetLysGluValGluAlaValValValAlaAlaLeuSerGlyLysSerSerGlySer 163
                                                                                 TCAAGCACTTCTTCCGAGGAAACTTCAACAACTGATTCCTCCGAACAACCTTCAAGCACT 464
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/clone="BA0AB037D05"
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                                                                                                                 This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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Bernot,A., Fizames,C., Wincker,P.,
Saurin,W. and Weissenbach,J.
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GSS; genome survey sequence
Tetraodon nigroviridis
Tetraodon nigroviridis
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/db_xref="taxon:99883"
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/note="Genoscope sequence ID : COAAO1OACO4A1~end

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TCCCGTACGGCGGGAATATCTCAATCAGCCAGCCAGCATGGCTCCACTGCTTCTAGTATT 694
                                      SerThrProGlnGlyValProGlnGlnAspLysLeuSerGlyAsnGluThrLysGlnIle 44
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de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Liorente,B.,
Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
Saurin,W., Tekaia,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
FEBS Lett. 487 (1), 3-12 (2000)
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Pichia angusta
Eukaryota; Fungi;
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of Pichia angusta, genomic survey sequence.
AL431231
AL431231.1 GI:12214643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces Kluyveromyces Saccharomyces Kluyveromyces thermotolerans, Kluyveromyces marxianus var. marxianus, Pichia lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia sorbitophila, angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
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Blandin, G., Llorente,
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/clone="BBOAA002G01"
/clone_lib="BBOAA"
/note="end : T7"
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/strain="CBS 4732"
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                                                                                                                                   Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M., Wincker, P. and Weissenbach, J. Genomic exploration of the hemiascomycetous yeasts: 1. A set o yeast species for molecular evolution studies FEBS Lett. 487 (1), 3-12 (2000)
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Bolotin-Fukuhara,M., Toffano-Nioche,C., Artiguenave,F., Duchateau-Nguyen,G., Lemaire,M., Marmeisse,R., Montrocher,R., Robert,C., Termier,M., Wincker,P. and Wesolowski-Louvel,M.
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Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
Location/Qualifiers
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FEBS Lett. 487 (1), 3-12 (2000)
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Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: seqref(genoscope.cns.fr - Web: www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen
                                                                                                                                                                                                                                                                                                                                                                                    Casaregola, S., Neuveglise, C., Lepingle, A., Bon, E., Feyn Artiguenave, F., Wincker, P. and Gaillardin, C. Genomic exploration of the hemiascomycetous yeasts: 17.
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GSS; genome survey sequence. Tetraodon nigroviridis. Tetraodon nigroviridis
                                                                                                                      Tetraodon nigroviridis genome survey sequence PUC-Ori end of 231NO2 of library G from Tetraodon nigroviridis. Genomic commonses
                                           AL178917.1 GI:7816974
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/note="Organ: skin; Vector: pBluescript SK-; Site_1:
/note="Cryan: skin; Vector: pBluescript SK-; Site_1:
/note="Cryan: skin; Vector: pBluescript SK-; Site_1:
/note="Cryan: Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Still Stil
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/clone_lib="Stratagene mouse
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/dev_stage="11 weeks old"
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/strain="C57BL/6"
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                                                                                                                                      Tetraodon nigroviridis, genomic survey
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US-09-889-314-2 (1-496) x CNS02310 (1-809)
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---AlaAspThrGlyValSerGlyAlaAlaAlaThrThrAlaSerAsnThrAla-ThrLy 116
                                                                                  sIleAlaMetGlnThrSerIleGluGluAlaSerLysSerMetGluSerThrLeuGluSe 136
                                                                                                                            GAGGGGCAAACCGGGGGGGGGGGGGGCGCACCSGCCCAGGVGGACCGGAGCACAGCSGACCRC 315
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Human gene number cottage.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission Submitted (12-APR-2000) Submitted (12-APR-2000) This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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Roest-Crollius, H.,
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/clone="231NO2"
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lt,A., Quetier,F., Saurin,W., Bernot
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Mismatches:
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US-09-889-314-2 (1-496) x BC028951 (1-2589)
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                                                                                                                                                       251
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aValGlyAlaAlaAlaGlyGlyAlaAlaGlyAlaAlaAlaAlaThrThrValAlaTh 311
                                                                       rIleValAlaAlaIlePheThrCysGlyAlaGlyLeuAlaGlyLeuAlaAlaGlyAlaAl
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                                          C----
                                                                                                                                                                                                                                                                   AACTCAGACGCCCCAGCCTGCTCAGGTGGCCTTGGCAAAGCCTCCGGTG------
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                                                                                                                                                                                                                                                                                                                                                                                                                 CCCACGGCCTGGGGCTTTGCTCACAGGCACCACAGTG---ACCAACCTTCAGGTGGCCCG
                                                                                                                                       yThrMetAspThrValAsnThrValMetI1eAlaValSerValAlaI1eThrValI1leSe
                                                                                                                                                                                                                           sGluArgGluGluTyrGlnGluMetLysAlaAlaGluGlnLysSerLysAspLeuGluGl 251
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This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/db_xref="taxon:10990"
/clone="IMAGE:5364153"
/tissue_type="Eye, retina, mouse st
/clone_lib="NHH_MGC_94"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
/note="Vector: pCMV-SPORT6"
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JOURNAL COMMENT	KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS	RESULT 18 AA930444/c LOCUS DEFINITION ACCESSION	Qy Db	Qу Db	Qу Дъ	Qy Db	Qy Db	Qy Db	Qy Db	Qy Db	Qy Db	DЬ
AL		18 44/c TION SION	466 902	446	426 I	410 : 728 (	390 I	371 : 653 :	351 : 603	331 · 596 ·	311 545	485
EST Project School of ay, Box 8	horda odent Alle Lacy toe, M	Stratagen 612 5' sim PE II.4. ;	rGlnLysAlaThrLysLeuGlyAlaGlnIle 476 :::              ::: CACACAGGCAACGGCAACAGGTA 932	nPheTrpGlnGlnAlaSerLysIleAlaSerLysGlnThrGlyGluSerAsnGluMetTh 466                      :::    TATACAACAAGTTGCATCAGCTTCTCAGCAGGCCTTCTCCACAGACGGTGACGCT 901	nPheGlnLysGluValGlyLysLeuGlnAlaAlaAlaAspMetIleSerMetPheThrGl 446	sGlyIleMetGlnMetGlnLeuSerGluMetGlnGln	uThrSerLysTrpValThrValGlyValGlyValValValAlaAlaProAlaLeuGlyLy 410	sGlyThrGlnMetIleAlaLysAsnPheProLysLeuSerLysValIleSerSerLe 390	STHTLeuValLysAlaIleAlaLysAlaIleSerLysGlyIleSerLysValPheAlaLy 371	gGlnAlaIleThrAlaAlaIleLysAlaAlaValLysSerGlyIleLysAlaPheIleLy 351     ACAGCAG602	rGlnIleThrValGlnAlaValValGlnAlaValLysGlnAlaValIleThrAlaValAr 331 ::       ::::::: ::	

335	AlavalIleThrAlavalArgClnAlaIleThr	325	Qy
2536	GTTGAATGAGTTGACCCAGCTCAAACAACTGGTGGATGCACAAAAAGAG	2477	В
324	ThrValGlnAlaValValGlnAlaValLysGln	307	Qy
306 2476	AlaGlyAlaAlaValGlyAlaAlaAlaGlyGlyAlaAlaGlyAlaAlaAlaAlaAla:	288 2417	Оу
287 2416	la TG	272 2357	Db Oy
2356	 	9	B 2
271	ThrVallleser	268	Q
267 2296	AspLeuGluGlyThrMetAspThrValAsnThrValMetIleAlaValSerValAlaIle::::	248 2237	Db Qy
2236	GAAGAAATCATGAAATTAAAAGACACACTAAAAAGTCAGATGACACAGGAAGCCAGTGAT	2177	망
247	GluGlnLysSerLys 2	243	Qy
2176	GTTATTGAGAATATGAATAAGGAGAAAGCATTTTTGTTTG	2117	망
242		242	Qy
2116	TATTGCTCT	2057	В
242		232	Qy
2056	AlaGlnAlaAspGlnThrAsnLysLeuGlyLeuGluLysGlnAlaIleLysIleAspLys 2 ::::: ::::: :::	212 1997	Db
9	TAAAGCAGGATCTGCAGAATGCATTAGAAGAA	1937	рь
211	AlaSerThrGln 2	208	Qy
1936	::: TTGTCTCACCT	1880	Дb
207	Thr	194	Qy
193 18 <b>7</b> 9	ProGlyValThrProArgSerGluValIleGluIleGlyLeuAlaLeuAlaLysAlaIle 1::::::::::::::::::::::::::::::::::::	174 1820	дь VQ
819	TCAGAGAACAGCTCTGACCTCAGCCAGAAACTTAAA 1	1778	В
73	euGluThrProGluLeuProLys 1 	155	Оy
.777	::: TTAAACAACACT 1	1718	DЬ
.54	alAla 1	137	Ωу
1717	AGAGCTCTGAAGCAGAGAGA	1658	망
136	lnThrSerIleGluGluAlaSerLysSerMetGluSerThrLeuGluSer	118	Qy
657	CCATCTGTCTTAATACATTCTTTAGGTAAATCCACTACTGACAATGATGTCAGAATTCAG 1	1598	DЪ
117	rAlaSerAsnThrAlaThrLysIle	98	Qy
597	ThrAlaProGlnGlnGlyValAlaAlaGlyLySGluSerSerGluSerGlnLySAlaGly 9	78 1541	р
540	:: AC 1	1502	Db

Clone distribution:  $\mbox{MGC}$  clone distribution information can be

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TITLE
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                                                                                                                                                                                                                                                                 Strausberg,R.

Direct Submission

Submission

Submitted (01-MAY-2002) National Institutes of Health, Mammalian Submitted (01-MAY-2002) National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
Gunaratne, P.H., Garcia, Yoon, V.S., Kowis, C.R., Richards, S., Gibbs, R.A
                                                                                                                           cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genom
                                                                                                                                                                                NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: The Cepko Laboratory
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IMAGE:5364153,
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                                                        Contact: amg@bcm.tmc.edu
                                                                         Web site: http://www.hgsc.bcm.tmc.edu/cdna/
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Lawrence,
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                    Hulyk, S.W., Hale, S. Martin, R.G., Muzny,
                                                                                                                                   Genome
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{\tt AspAlaThrIleAlaGlyAlaSerGlyLysAspLysThrSerSerThrThrLysThrGlu}
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Homo sapiens, retinoic acid induced 14, clone IMAGE:4822221, mRNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at: http://image.llnl.gov series: IRAK Plate: 33 Row: c Column: 23 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 13470085 This clone has the following problem: frame shifted.
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Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
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Anup Madan, Jessica Fahey, Erin He
Madan, Stephanie Rodrigues, Amy Sa
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Tissue Procurement: Miklos Palkovits,
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Contact: MGC help desk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5, GAGAGAGAGAGTCCAAGAGCTCTTTTTTTTTTTTTTTVN 3,], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehin-ro-cho, Tsurumi-ku, Yokoha Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wynshaw-Boris, A., and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI.
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/clone="2900019J01"
                                                                                                                                                                                             /protein_id="BAB28906.1"
/db_xref="GI:12850969"
                                                                                                                                                                                                                                                                                                             /note="DNA segment, KIST
data source:MGD, source }
                                                                                                                                                                                                                                                                                                                                                                   /gene="D0Kist6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="male"
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AL534303
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BP 191 91006 EVRY cedex - Franc
Email: segref@genoscope.cns.fr,
                                                                                                                                                                                                                                   Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                 Mammalia; Eutheria;
1 (bases 1 to 1194)
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                                          /clone_lib="LTI_FL013_FBrn1"
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week, 24 week and 26 week)"
                                                                                          /db_xref="taxon:9606"
/clone="CS0DF005YK24"
              /note="Organ: Fetal brain; Vector:
                               /lab_host="DH10B"
                                                                                                                         organism="Homo sapiens"
                                                                                                                                                         ocation/Qualifiers
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Percent Similarity:
Best Local Similarity:
Query Match:
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tLysAlaAlaGluGlnLysSerLysAspLeuGluGlyThrMetAspThrValAsnThrVa 259
                                                                                                                                                                                                    aThrLysSerAlaLeuSerAsnTyrAlaSerThrGlnAlaGlnAlaAspGlnThrAsnLy
                                                                                                    {\tt sLeuGlyLeuGluLysGlnAlaIleLysIleAspLysGluArgGluGluTyrGlnGluMe}
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a 170 c 272 g 121 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 was blunt end-repaired with T4 DNA polymerase.
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Tel: 801 585 5606  Fax: 801 585 7177  Email: ddunn@genetics.utah.edu Insert Length: 10000	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts Unpublished (2001) Contact: Robert B. Weiss University of Utah Genome Center University of Utah Genome Center University of Utah Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA	iN0463X14R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0463X14 R, DNA sequence. AZ624776. AZ624776.1 GI:11747062 GSS. house mouse. Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Musmyota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus. Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus. 1 (Dases 1 to 746) Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Welss,R.	rGlnLysAlaThrLysLeuGlyAlaGlnIleLeuLysAlaTyrAlaAlaIleSerGlyAl 486 ::::::	nLysGluValGlyLysLeuGlnAlaAlaAspMetIleSerMetPheThrG1 446	eAlaLysGlyThrGlnMetIleAlaLysAsnPheProLysLeuSerLysValIleSerSe 389

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                                                                                                                                                                             Homo sapiens,
BC016144
BC016144.1 GI
Submitted (22-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11AO3, Bethesda, MD 20892-2590,
                                                                                                                                               Homo
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                                                                Strausberg, R.
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                                                Direct Submission
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                                                                             ; Metazoa; Chordata; Eutheria; Primates; 1 to 4272)
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clone IMAGE:3921754,
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lSerGlyAlaAlaThrThrAla---SerAsnThrAlaThrLysIleAlaMetGlnTh
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                                          AAAAATTCTCCAGGTCAGAGCTGCCTCAGCCCCTGCCAAG--
                                                                              nGlyValAlaAlaGlyLysGluSerSerGluSerGlnLysAlaGlyAlaAspThrGlyVa 102
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Tissue Procurement: ATCC/DCTD/DTP
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can through the I.M.A.G.E. Consortium/LLL at: http://image.llr Series: IRAK Plate: 15 Row: n Column: 1
This clone was selected for full length sequencing because
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
NIH-MGC Project URL: http://mgc.nci.nih
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 passed the following selection criteria: matched mRNA gi: 4507410 This clone has the following problem: frame shifted.
                                                                                                                                                                                                                                              --IleGlnGlnThrArgGlnGlyLysAsnThrGluMetGluSerAspAlaThrIleAl
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/note="Vector: pCMV-SPORT6"
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/clone_lib="NIH_MGC_72"
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                                                                                                             Coe,
                                                            Submitted (25-APR-2002) Maize Mapping Missouri, Columbia, MO 65211, USA Location/Qualifiers
                                                                                                                                                                              1 (bases 1 to 1845)
Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.
                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
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AY103583
AY103583.1 GI:21206661
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        /organism="Zea mays"
/db_xref="MaizeDB:636617"
/db_xref="taxon:4577"
/clone="PC0113569"
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                                                                                                                     Submitted (08-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                              NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                         Strausberg, R.
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cgapbs-r@mail.nih.
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Percent Similarity:
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Contact: nisc_mg(sin, nin, gov)

Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,

Blakesley,R.M., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,

Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,

Hansen,N., Ho,S.-L., Karlins,E., Laric,P., Legaspi,R., Maduro,Q.L.,

Masiello,C., Maskeri,B., Mastrian,S.D., McDloskey,J.C., McDowell,J.,

Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Tsurgeon,C.,

Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A.,

Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clone distribution: MGC clone distribution information can be for through the I.M.A.G.B. Consorthum/LLNL at: http://image.llnl.gov Series: IRAK Plate: 62 Row: n Column: 10 This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
cNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
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/tissue_type="Brain, fetal,
/clone_lib="NIH_MGC_121"
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                                                                                                                                      AlaAlaAla-----AlaGlyGlyAlaAlaGlyAlaAlaAlaAlaThrThrValAlaThr
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                                             AGCGTT 538
                                                                                                         GCTGCTGCTGAGGATGCTTCTGGAGCTGCTGGAGCTGCTTCTGGAACCACCGCTCCCGAG
                                                                                                                                                                                                                                                                                                                          TyrGlnGluMetLysAlaAlaGluGlnLysSerLysAspLeuGluGlyThrMetAspThr 255
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KEYWORDS
SOURCE
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                                                                                                                                                                                            Query Match:
                                                                                                                                                                                                                 Best Local Similarity:
                                                                                                                                                                                                                                                          Score:
                                                                                                                                                                                                                                                                            Pred.
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                                                           154
                    76
                                                                                                56
                {\tt ThrGluThrAlaProGlnGlnGlyValAlaAlaGlyLysGluSerSerGluSerGlnLys}
                                                         GAATCCGATGCA-----TCTGCCACTTCTGGTGTTTCATCTGCTTCTGATGCTAGTGAA
                                                                             GluSerAspAlaThrIleAlaGlyAlaSerGlyLysAspLysThrSerSerThrThrLys 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEBS Lett.
20584726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Souciet, J.L., Aiglé, M., Artiguenave, F., Blandin, G., Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S., de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B., Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S., Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M., Wincker, P. and Weissenbach, J. Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies
FEBS Lett. 487 (1), 3-12 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CNS07CG2 938 bp DNA linear GSS 08-JI
T7 end of clone BD0AA002F07 of library BD0AA from strain CBS
Candida tropicalis, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 kb were prepared and both extremities were sequenced. keywords for description of this sequence and for the set the other extremity of this insert.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              segref@genoscope.cns.fr - Web :
This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
yeast species: Saccharomyces servazzii, Zygosaccharomyces rouxii,
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE: (E-mail
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AL439128.1 GI:12222541
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/strain="CBS 94"
/db_xref="taxon:5482"
/clone="BD0AA002F07"
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/note="end : T7"
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GluGluTyrGlnGluMetLysAlaAlaGluGlnLysSerLysAspLeuGluGly---Thr 252
                                                                                                                                                                  GlnThrSerIleGluGluAlaSerLys-----
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                                                         AspGlnThrAsnLysLeuGlyLeuGluLys---GlnAlaIleLysIleAspLysGluArg
                                                                                                                   ThrLeuGlyGluAlaThrLysSerAlaLeuSerAsnTyrAlaSerThrGlnAlaGlnAla 214
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Location/Qualifiers
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/strain="CBS 4732"
/db_xref="taxon:4905"
/clone="BBOAA002F11"
/clone_lib="BBOAA"
/note="end : T3"
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                              -GGTTTGAGCTCTGCCGCTGCCATATCAGGCTCCAACTCTGCC
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IMAGE:3844335,
BC016304
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Direct Submission
Submitted (29-OCT-2001) National Institutes of Health, Mammalian Submitted (29-OCT-2001), Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Trastitute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
                                                                                                                                                                                                                                                                                                                                                                    through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 25 Row: b Column: 20
This clone has the following problem: frame shifted.
Location/Qualifiers
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Tissue Procurement: ATCC
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Contact: MGC help desk
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                                                                                                        /tissue_type="Placenta,
/clone_lib="NIH_MGC_21"
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Contact: Wan KL
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Comparative EST analyses provide insights into gene
two asexual developmental stages of Eimeria tenella
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PCR PRimers
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                                                                                                       Direct Submission

Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: sequefgenoscope.cns.fr - Web: www.genoscope.cns.fr)

This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
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45 w. Gude Dr.,
Tel: 2404533151
Fax: 2404534580
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Contact: Holt R.A.
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Holt.R.A., Lin,J.-J., Murphy,S.D., Evans,C.A.,
.R., Collins,F.H., Venter,J.C. and Hoffman,S.L.
Celera Anopheles gambiae EST project
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
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primer: M13 Reverse.
                 305
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              /note="vector: psport1; Site_1: Sal1; Site_2: Not1; Whole adult mosquitoes (mixed sex) frozen on liquid nitrogen 2 hours after human blood feeding. cDnA inserts >500 bp cloned directionally into psport 1. Not 1 site is 3'. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)" a 234 c 135 g 37 t
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/strain="RSP-ST (Reduced
chromosome)"
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/clone="19600449697628"
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GAAGCTTCATCCATCTTGGATGAGGGGCAGCAGCTCTGGCTC
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                                               AGCGTCCCTGCTTCCACACCCACCCACGGGTGGAGCCAGAGTGACTGAGTGAATATTTCAG
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                                      MetAspThrValAsnThrValMetIleAlaValSerValAlaIleThrValIleSerIle
                                                                              ArgGluGluTyrGlnGluMetLysAlaAlaGluGlnLysSerLysAspLeuGluGlyThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Bouneau, L., Billault, A., Quetler, F., Saurin, W., Bernot Weissenbach, J.
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Human gene number estimate provided by genome wide analysis using Tetracoon nigroviridis DNA sequence
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.

1 (bases 1 to 935)
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/clone_lib="G"
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VERSION KEYWORDS JOURNAL REFERENCE AUTHORS REFERENCE AUTHORS DEFINITION JOURNAL REFERENCE AUTHORS TITLE JOURNAL ACCESSION SOURCE ORGANISM TITLE TITLE

AL225985
AL225985.1 GI:7884892
AL225985.1 GI:7884892
GSS; genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis. CNS033D4 935 bp DNA linear GSS 15-MAY-2000 Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 208D22 of library G from Tetraodon nigroviridis, genomic survey

Tetraodon.

2 (bases 1 to 935)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
unpublished Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottler, P., Quetier, F., saurin, W. and Weissenbach, J. saurin, W. and Weissenbach, J. Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tet.

1 (bases 1 to 935)

Genoscope.
Direct Submission (bases 1 to 935)

COMMENT

Submitted (12-APR-2000) read and was generated as part of a large This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.

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                                   AlaSerAsnThrAlaThrLysIleAlaMet-----GlnThrSerIleGluGluAla 126
                                                                                           LysAlaGlyAlaAspThrGlyValSerGlyAlaAla---
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This GSS is part of a random genomic sequencing program of thirtee yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyce
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Pichia angusta
                                                  Genomic exploration of the hemiascomycetous yeasts: yeast species for molecular evolution studies
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CNS07CJY LOCUS DEFINITION

CNSO7CJY 936 bp DNA linear GSS 08-JUL-2001 T7 end of clone BD0AA003E07 of library BD0AA from strain CBS 94 of Candida tropicalis, genomic survey sequence.

ALIGNMENTS

KEYWORDS SOURCE ORGANISM ACCESSION VERSION

Candida tropicalis

GSS AL439268

AL439268.1 GI:12222681 Candida tropicalis.

REFERENCE

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharosaccharomycetales; mitosporic Saccharomycetales; Candida 1 (bases 1 to 936) Souciet, J. L., Aigle, M., Artiguenave, F., Blandin, G., Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,

Saccharomycetes;

Candida

AUTHORS

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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